

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:50:20 ; Search time 7570.62 Seconds  
(without alignments)  
10778.327 Million cell updates/sec

Title: US-10-085-233B-1

Perfect score: 1684  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:  
1: gb ba: \*  
2: gb bkg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472.6	87.4	2525	6	AX147836 Sequence
2	1472.6	87.4	2525	6	AX521885 Sequence
3	1472.2	87.4	113306	6	AX646815 Sequence
4	1472.2	87.4	218186	9	AC083865 Homo sapi
5	1462.6	86.9	162268	9	AC146385 Pan trogl
6	1228.6	73.0	1336	6	AX709193 Sequence
7	1106.2	65.7	1340	6	AX709194 Sequence
8	1106.2	65.7	1460	6	AX709195 Sequence
9	1030	61.2	1499	6	AX451925 Sequence
10	991.2	58.9	1051	6	AX453412 Sequence
11	930.4	55.2	1332	6	CQ737895 Sequence
12	916.4	54.4	918	6	BD187510 Novel Pol
13	916.4	54.4	918	6	AX481576 Sequence
14	916.4	54.4	918	6	AX498180 Sequence
15	916.4	54.4	918	6	BD105324 Novel G p
16	916.4	54.4	918	6	AX288420 Homo sapi
17	884.2	52.5	140539	2	AC079758 Homo sapi
18	725.6	43.1	206999	10	AC122886 Mus muscu
19	690	41.0	972	6	AX657538 Sequence

C	20	639.6	38.0	167316	2	AC078995	AC078995 Mus muscu
C	21	634.8	37.7	918	10	AY288427	AY288427 Mus muscu
C	22	605.2	35.9	228766	2	AC099132	AC099132 Rattus no
C	23	456	27.1	456	9	AY25538	AY25538 Homo sapi
C	24	433	25.7	744	10	AY288432	AY288432 Rattus no
C	25	404.4	24.0	447	6	AX147776	AX147776 Sequence
C	26	404.4	24.0	447	6	AX521825	AX521825 Sequence
C	27	275.2	16.3	393	10	AY255553	AY255553 Mus muscu
C	28	184	10.9	169155	5	EX088685	EX088685 Zebrafish
C	29	184	10.9	173882	5	EX640462	EX640462 Zebrafish
C	30	152.2	9.0	162925	2	AC018528	AC018528 Homo sapi
C	31	152.2	9.0	165120	9	AC083860	AC083860 Homo sapi
C	32	144.8	8.6	897	6	BD182016	BD182016 Homo sapi
C	33	131.4	7.8	187649	9	AC146213	AC146213 Pan trogl
C	34	103.4	6.1	140539	2	AC079758	AC079758 Homo sapi
C	35	103.4	6.1	225912	2	AC084210	AC084210 Homo sapi
C	36	76.4	4.5	1113	6	AX280917	AX280917 Sequence
C	37	76.4	4.5	1113	9	AY268428	AY268428 Homo sapi
C	38	76.4	4.5	1113	9	CR542082	CR542082 Homo sapi
C	39	76.4	4.5	1252	9	HUMODRLP	140949 Homo sapien
C	40	76.4	4.5	1379	9	AF348323	AF348323 Homo sapi
C	41	76.4	4.5	1805	6	AX746239	AX746239 Sequence
C	42	76.4	4.5	1973	6	AR270828	AR270828 Sequence
C	43	76.4	4.5	1973	6	AR380872	AR380872 Sequence
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C	45	76.4	4.5	2534	6	AX548923	AX548923 Sequence

#### ALIGNMENTS

RESULT 1	AX147836	Sequence 81 from Patent WO0136473.	2525 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX147836					
DEFINITION	AX147836					
ACCESSION	AX147836.1	GI:14346839				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
1	Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kayes, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T., and Huff, R.M.					
TITLE	Novel 9 protein-coupled receptors					
JOURNAL	Patent: WO 0136473-A 81 25-MAY-2001;					
PHARMACIA & UPJOHN COMPANY (US)						
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ORIGIN						
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Best local Similarity	99.6%	Pred. No. 0;				
Matches 1497;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 2;		
Db	153	AAATGTGACTTCCCAAGTAACTGCTGGCCAAATACCTCCAGAAATCTCTTGGCATCTT	212			
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Db	213	ATATGTGACCCCACTTAATCAGCTCTCTACTTCAATGATGCTTATTTGGCGGGGTGAGGT	272			
Qy	69	ATATGTGACCCCACTTAATCAGCTCTCTACTTCAATGATGCTTATTTGGCGGGGTGAGGT	128			
Db	273	GTCATTTCACTTCTTTCTCTCTCTGTTGAATAAGAACCCCGTCACTGACCAACATGCGC	332			
Qy	129	GTCATTTCACTTCTTTCTCTCTCTGTTGAATAAGAACCCCGTCACTGACCAACATGCGC	188			
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Db 249 TACCTCATCAAGAAAGACTTGGATGTGGGGCTGCCCTTCGCAAAATTTGAGTGCATG 308  
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Db 309 CTGCACATCCACATGTACTCAGCTTCTTAATTCATGTGGGAAATCCGTGACACAGATAC 368  
Qy 513 CTGATCTTCTTCAAGTCCAAAGACAAAGTGAAATTTACAGAAAATCGCATGCTGTGCT 572  
Db 369 CTGATCTTCTTCAAGTCCAAAGACAAAGTGAAATTTACAGAAAATCGCATGCTGTGCT 428  
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Db 429 GCCAGTCTGGCATGTGAGAGCGTGTGATGTGATCTGTGGTACCCCTGTTGTCTCCCG 488  
Qy 633 TATGGAATCCATGAGAAATCAATGAGAGACGTTTAAATTTCACAAAAGCTTGTCT 692  
Db 489 TATGGAATCCATGAGAAATCAATGAGAGACGTTTAAATTTCACAAAAGCTTGTCT 548  
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Db 969 GCTTCCTTATATTTGGGAATAAAAATGGTATATAGGGAGGTAAAGATGTTCATTAC 1028  
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Qy 1592 GGAGAAATGATTAATAAATTTTCTAGGGTATCAATCTGTGTAGAAATGATCTGTCT 1651  
Db 1448 GGAGAAATGATTAATAAATTTTCTAGGGTATCAATCTGTGTAGAAATGATCTGTCT 1507  
Qy 1652 AGA 1654  
Db 1508 AGA 1510

RESULT 2  
AX521885  
LOCUS  
DEFINITION  
Sequence 81 from Patent W02064789.  
AX521885  
ACCESSION  
AX521885.1 GI:24410791  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1  
Lind, P., Parodi, L. A., Vogel, G. and Wood, L. S.  
G protein-coupled receptor  
Patent: WO 02064789-A 81 22-AUG-2002;  
PHARMACIA & UPJOHN COMPANY (US)  
Location/Qualifiers  
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FEATURES  
source

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Query Match 87.4%; Score 1472.6; DB 6; Length 2525;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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QY 1652 AGA 1654  
DB 1508 AGA 1510

RESULT 3  
LOCUS AX646815  
DEFINITION Sequence 1007 from Patent EP1270724.  
ACCESSION AX646815  
VERSION AX646815.1  
KEYWORDS GI:28799225  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.  
TITLE Guanosine triphosphate-binding protein coupled receptors  
JOURNAL Patent: EP 1270724-A 1007 02-JAN-2003;  
National Institute of Advanced Industrial Science and Technology (JP) ; Center for Advanced Science and Technology Incubation, Ltd. (JP)

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ORIGIN  
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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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DB 11764 CCTCATCAAGAAGACTTGAATGTTTGGGCTGCCCTCTGCAAAATTTGTGAGTCCATGCT 11823  
QY 455 GCACATCAACATGATCTTCAAGTCTTATTTATGTTGATCTGTGATCAACGATACCT 514  
DB 11824 GCACATCAACATGATCTTCAAGTCTTATTTATGTTGATCTGTGATCAACGATACCT 11883  
QY 515 CATCTTCTTCAAGTGAAGAAAGTGAATTTCTACAGAAAACATGATGCTGTGCTG 574

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Qy	935	CAATGCCGTAGACGACGAAGGTGATTTTATAAGAAATCTTCTAGAGTAAACACAAAT	994
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Qy	1294	TTGAATCACCTGAGGTGCATATTTAATTAATTAATTTTTCAGTACAGATGTCTGTGTGGCC	1353
Db	12664	TTGAATCACCTGAGGTGCATATTTAATTAATTAATTTTTCAGTACAGATGTCTGTGTGGCC	12723
Qy	1354	CATGAAGAACAATAGGTTTTTAAGAGTTTNAAGATTTCAATAGTCATTTTAAGTTCTT	1413
Db	12724	CATGAAGAACAATAGGTTTTTAAGAGTTT-AAAAGTTTCAATAGTCATTTTAAGTTCTT	12783
Qy	1414	CTGTTTGAAGCATGTCCTTAAAGTTTGTGGACTGAACTCAGACCTTTAGTTCTTTTCAATC	1473
Db	12783	CTGTTTGAAGCATGTCCTTAAAGTTTGTGGACTGAACTCAGACCTTTAGTTCTTTTCAATC	12843
Qy	1474	CCACTTACCAATAGTAAATTTCTGGCCCAACCCAGCTCCAAAGACACAACTCTTC	1533
Db	12843	CCACTTACCAATAGTAAATTTCTGGCCCAACCCAGCTCCAAAGACACAACTCTTC	12902
Qy	1534	CTTGCTTAACAGGTTATGATGTCCCATTTATCTCAGCCCTGATATAAACTGATAAGGGG	1593
Db	12903	CTTGCTTAACAGGTTATGATGTCCCATTTATCTCAGCCCTGATATAAACTGATAAGGGG	12962
Qy	1594	AGAAATAGTTAAATTTTCTTACGGGTATCATTACTCTGTGAGAAATCATCTGTCTAG	1653

Db 12963 AGAGATAGTAAAAATTTTCTAGGGTATCATPACTCTGGTAGGAGTCATCTGTCTAG 13022

QY 1654 A 1654

Db 13023 A 13023

RESULT 4	
AC083865	AC083865      218186 bp    DNA      linear    PRI 26-JAN-2001
LOCUS	Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION	AC083865
VERSION	AC083865.2    GI:12545315
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS  
1 (bases 1 to 218186)  
Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and

TITLE	Large-scale Mapping and Sequencing of Human Chromosome 7
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 218186)
AUTHORS	Kaul, R., Olson, M. V., Raymond, C., Clendenning, J. and Haugen, E

**JOURNAL** Submitted (04-OCT-2000) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
**REFERENCE** 3 (Pages 1 to 21816)  
**AUTHORS** Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and  
Olson, M.V.

**JOURNAL** Submitted (26-JUN-2001) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
**COMMENT** On Jan 26, 2001 this sequence version replaced gi:10567930.

Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: <http://www.genome.washington.edu>  
Contact: uwgchgs@u.washington.edu

```

----- Project Information -----
Center project name: HsaChr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics -----

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Sequencing vector: plasmid; X52328; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 217693 bases at least Q40  
Consensus quality: 218145 bases at least Q30  
Consensus quality: 218186 bases at least Q20  
Insert size: 273875; 19.1% error; agarose-fp  
Insert size: 218186; sum-of-contigs  
Quality coverage: 8..30x in Q20 bases; agarose-fp  
Quality coverage: 10..42x in Q20 bases; sum-of-contigs

### Overlapping Sequences:

5': mapping in progress  
3': RP11-243E12 (UMGC:djs156) AC018634, 6468-bp overlap

**Sequence Quality Assessment:** This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing



problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

#### Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt
8696	8979	764	755	3414	3439
6	<800	6382	6611	2067	2102
663	<800	512	<800	5356	5585
122	<800	449	<800	1416	1421
174	<800	1059	1063	610	<800
4551	4612	70	<800	225	<800
952	988	424	<800	932	961
968	988	2594	2670	1982	2102
980	988	3852	3908	29	<800
10043	10231	915	918	2663	2719
2412	2471	5333	5315	5958	5921
3670	3625	4795	4869	448	<800
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27	<800	552	<800	1869	1948
9749	10231	1010	1063	3655	3640
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57	<800	13428	13500	2139	2102
2128	2184	12540	12591	1593	1527
1087	1101	4819	4869	2049	2102
2839	2805	11280	11329	614	<800
2787	2805	840	918	7901	8084
5407	5309	9244	8985	619	<800

3324	3348	1672	1707	5583	5585
7246	7468	3195	3163	345	<800
4508	4455	4273	4301	324	<800
5815	5866	1980	2031	1496	1421
5380	5309	520	<800	6710	6637
349	<800	737	755	71	<800
4509	4612	1833	1878	848	877
571	<800	8798	8985	6153	6135
4162	4455	2024	2031	4085	4113
956	988	4946	4869	14	<800
2026	2123	6247	6163	44	<800
1821	1788	685	<800	10402	10380
2453	2471	1367	1406	300	<800
8955	9499	109	<800	5150	5294
1004	988	3608	3535	3195	3246
7399	7468	7728	7736	2281	2309
7516	7468	4264	4301	2740	2804
4119	4107	357	<800	5869	5921
193	<800	3645	3709	248	<800
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7034	7468	5668	5588	585	<800
4940	4902	957	918	655	<800
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761	<800	201	<800	1723	1693
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4086	4107	709	<800	2331	2309
5916	5835	4907	4869	1940	1993
6995	6947	1161	1195	5574	5585
4667	4612	11292	11329	3867	3865
10434	10231	6699	6611	1268	1270
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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 155 ATGTGACTTCCCAAGTATGCTGGCCACATATCTTCAGGAATTCCTTGGATCTAT 214  
DB 133107 AGGTGACTTCCCAAGTATGCTGGCCACATATCTTCAGGAATTCCTTGGATCTAT 133166  
QY 215 AGTGAACCCCACTTATACGCTTACTTATGCTTATTTGGCGGCTGTGGATGT 274

Db 133167 AGGACACCCACCTTAATGAGCCCTCTACTCATATGTCCTATTTGGCGGCGTGTGGGTGT 133226  
Qy 275 CATTCGATCTTTTCTCCGTGGGAAATGAACACCGGTCAGTGCACCAATGGCGGT 334  
Db 133227 CATTCGATCTTTTCTCCGTGGGAAATGAACACCGGTCAGTGCACCAATGGCGGT 133286  
Qy 335 CATTAACCTGTTGGTGTCCACAGCGTTTCTGCTGACAGTGCATTTGGCTTGAACCTA 394  
Db 133287 CATTAACCTGTTGGTGTCCACAGCGTTTCTGCTGACAGTGCATTTGGCTTGAACCTA 133346  
Qy 395 CTTTCATGAAGAAGCTTGATGTTTGGGCGTCCCTTCTGCAATTTTGTGATGTCATGCT 454  
Db 133347 CTTTCATGAAGAAGCTTGATGTTTGGGCGTCCCTTCTGCAATTTTGTGATGTCATGCT 133406  
Qy 455 GCAATCATCAGATGATGCTGACGTTCTTAATCTAATGTTGATGCTGCTGACCAATATCT 514  
Db 133407 GCAATCATCAGATGATGCTGACGTTCTTAATCTAATGTTGATGCTGCTGACCAATATCT 133466  
Qy 515 CATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATCTACAGAAAATGCGATGCTGTGCTGC 574  
Db 133467 CATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATCTACAGAAAATGCGATGCTGTGCTGC 133526  
Qy 575 CAGTGTGCGCATGTGGACGCTGGTGAATGTCATTTGTGTCACCCCTGGTTGTCTCCCGGTA 634  
Db 133527 CAGTGTGCGCATGTGGACGCTGGTGAATGTCATTTGTGTCACCCCTGGTTGTCTCCCGGTA 133586  
Qy 635 TGGAAATCATGAGGAATGACAAATGAGAGCACTGTTTAAATTTCAAGAAAGCTGTGCTTA 694  
Db 133587 TGGAAATCATGAGGAATGACAAATGAGAGCACTGTTTAAATTTCAAGAAAGCTGTGCTTA 133646  
Qy 695 CACATATGTGAAAAATCATCAACTATATATGATATGATATGATATGATATGATATGATATGAT 754  
Db 133647 CACATATGTGAAAAATCATCAACTATATATGATATGATATGATATGATATGATATGATATGAT 133706  
Qy 755 TCTGTGTGTTCTTCCAGTCTTTCATCATATGTTGATGTTGTCAGAAAGCTACGCCATCTTT 814  
Db 133707 TCTGTGTGTTCTTCCAGTCTTTCATCATATGTTGATGTTGTCAGAAAGCTACGCCATCTTT 133766  
Qy 815 ACTATCCACACAGAGTTCTGGGCTCAGCTGAAACCTATTTTTTATAGGGGTCATCTT 874  
Db 133767 ACTATCCACACAGAGTTCTGGGCTCAGCTGAAACCTATTTTTTATAGGGGTCATCTT 133826  
Qy 875 TGTGTGTGTTCTTCCACAGTCTTCTTGAATCTATTAATGATGTTGTCAGCAATTC 934  
Db 133827 TGTGTGTGTTCTTCCACAGTCTTCTTGAATCTATTAATGATGTTGTCAGCAATTC 133886  
Qy 935 CAATGCTGTGACAGCAAGTTGATTTTAAAGCAATCTTCTGATGTCACAGCAAT 994  
Db 133887 CAATGCTGTGACAGCAAGTTGATTTTAAAGCAATCTTCTGATGTCACAGCAAT 133946  
Qy 995 TAGCTGTATGATTTGCTTCTTGTCTTGTGGGGGAAGCATTGGTTTAAAGCAAAAGAT 1054  
Db 133947 TAGCTGTATGATTTGCTTCTTGTCTTGTGGGGGAAGCATTGGTTTAAAGCAAAAGAT 134006  
Qy 1055 AATTTGCTTATGAAATGTTGTTGTCGCTTACCCCAAAATCAATCAATTCATTTATTTGC 1114  
Db 134007 AATTTGCTTATGAAATGTTGTTGTCGCTTACCCCAAAATCAATCAATTCATTTATTTGC 134066  
Qy 1115 TTCTCTTATATTTGGGAAT-AAAAATGGGTATAGGGAGGTAAAGATGATTTTCAATTT 1173  
Db 134067 TTCTCTTATATTTGGGAATAAAAATGGGTATAGGGAGGTAAAGATGATTTTCAATTT 134126  
Qy 1174 GATCAAAAACCATGCTGTATGTATCCCAAAACAAAGAGCTATATAATGCAAGAGCCCTCA 1233  
Db 134127 GATCAAAAACCATGCTGTATGTATCCCAAAACAAAGAGCTATATAATGCAAGAGCCCTCA 134186  
Qy 1234 TTGTAGTCTTATGGAATCCCTCCCATCTGATGATGAGCGGTACAAAGACCAAGTGTG 1293  
Db 134187 TTGTAGTCTTATGGAATCCCTCCCATCTGATGATGAGCGGTACAAAGACCAAGTGTG 134246  
Qy 1294 TTGAATCAGCTGAGTGTGCAATTTATGATTTTTCAGTACAGAAATGTCTGTGGCC 1353

Db 134247 TTGAATCAGCTGAGTGTGCAATTTATGATTTTTCAGTACAGAAATGCTGTGGCC 134306  
Qy 1354 CATGAAGAACAATAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT 1413  
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Qy 1414 CTTTGAAGACATGCTCTTGAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT 1473  
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Qy 1594 AGAATATGATTAATAATTTTCTAGGGTATCATTAATCTGTGATGAGAAATCATCTGTCTAG 1653  
Db 134546 AGAATATGATTAATAATTTTCTAGGGTATCATTAATCTGTGATGAGAAATCATCTGTCTAG 134605  
Qy 1654 A 1654  
Db 134606 A 134606

RESULT 5  
AC146385  
LOCUS AC146385 162268 bp DNA linear PRI 19-MAY-2004  
DEFINITION Pan troglodytes BAC clone RP43-126C6 from 7, complete sequence.  
AC146385.4 GI:46391241  
VERSION  
KEYWORDS HTG.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE  
AUTHORS Krushowski, S., Bielicki, L. and Haglund, K.  
TITLE The sequence of Pan troglodytes BAC clone RP43-126C6  
JOURNAL Unpublished (2001)  
AUTHORS Wilson, R.K.  
TITLE Direct Submision  
JOURNAL Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submision  
JOURNAL Submitted (22-FEB-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submision  
JOURNAL Submitted (15-APR-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submision  
JOURNAL Submitted (19-MAY-2004) Washington University School of Medicine,  
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
63108, USA  
COMMENT  
On Apr 15, 2004 this sequence version replaced gi:42734595.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@watson.wustl.edu  
----- Summary Statistics  
Center project name: C\_PT126C06

## NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPECI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Cline', Yerkes #C0471; birthdate: 6-6-80). The clone and detailed information can be obtained from Resgen (<http://www.resgen.com>) or Pieter de Jong and co-workers at <http://www.bacpac.chori.org>.

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC146047

Location/Qualifiers

1. 162268

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/chromosome="7"

/map="7"

/clone="RP43-126C6"

/clone\_1lb="RPECI-43"

138009..138038

unseqre

/note="Sequence derived from one plasmid subclone."

## ORIGIN

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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1490; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 155 ATGTGACTTCCCAAGTATGCTGCGCACAAATCTCCAGAAATTCCTTGCATCTCTAT 214
    |||
DB 146132 AGGTGACTTCCCAAGTATGCTGCGCACAAATCTCCAGAAATTCCTTGCATCTCTAT 146191
    |||

QY 215 AGTACACCCCACTTAATCAGCCTCTACTATAGTGTCTTATTTGGCGGGCTGGTGGGT 274
    |||
DB 146192 AGTACACCCCACTTAATCAGCCTCTACTATAGTGTCTTATTTGGCGGGCTGGTGGGT 146251
    |||

QY 275 CATTTCATCTTTTCTCTCTGTAATAATGAAACACCGGTCAGTGAACCAATGCGGT 334
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DB 146252 CATTTCATCTTTTCTCTCTGTAATAATGAAACACCGGTCAGTGAACCAATGCGGT 146311
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QY 335 CATTAACCTGGTGGTGCACAGCGTTTTCTGCTGACAGTGCACATTTGCTTGACCTA 394
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DB 146312 CATTAACCTGGTGGTGCACAGCGTTTTCTGCTGACAGTGCACATTTGCTTGACCTA 146371
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QY 395 CCTATCAAGAAGAATTGAGATTTGGGCTGCCCTTGCAGAAATTTGGAGTGCAGTCT 454
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DB 146372 CCTATCAAGAAGAATTGAGATTTGGGCTGCCCTTGCAGAAATTTGGAGTGCAGTCT 146431
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QY 455 GCACATCCACATGTAAGTCTCAATCTATATGATGATGATGATGATGATGATGATGAT 514
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DB 146432 GCACATCCACATGTAAGTCTCAATCTATATGATGATGATGATGATGATGATGATGAT 146491
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QY 515 CATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCAAGAAATCTGATGCTGGCTGC 574
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DB 146492 CATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCAAGAAATCTGATGCTGGCTGC 146551
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QY 575 CAGTGTGGGATGTGAGAGCGTGTGATTTGTCATTTGTGTATCCCTGGTGTCTCCGGTA 634
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DB 146612 TGAATCATGAGGAATATCAATGAGAGCACTGTTTTAAATTTCAACAAGAGCTTGCTTA 146671
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QY 695 CACATATGTAATAATCAATCAATATGATATGATATTTGTGCTATACCGTGTGAT 754
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QY 815 ACTATCCACACAGAGTTCGAGCTCAGCTGAATAAACTATTTTATAGGGTCACTCT 874
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QY 875 TGTGTTGTTTCTTCCCTACAGTTCCTTAGATCTATCTAGAAATGTTGATGAGCATTC 934
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DB 146972 TAGCTGTATGATTTGCTCTCTTGTCTTGGGGAGGCAATGTTTAAAGCAAAAGAT 147031
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QY 1055 AATTGGCTTATGGAATGTTGTTTGGCGGTAGCCCAAACTACATATTCATTTTGC 1114
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DB 147032 AATTGGCTTATGGAATGTTGTTTGGCGGTAGCCCAAACTACATATTCATTTTGC 147091
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QY 1115 TTCTTTATTTTGGGAAT-AAAATGGGTATAGGGAGATGAATGTTTCACTACTT 1173
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DB 147092 TTCTTTATTTTGGGAAT-AAAATGGGTATAGGGAGATGAATGTTTCACTACTT 147151
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QY 1174 GATCAAAACATGCTTATGATGATCAACCAAAACAAAGCAATTAATAATGCAAGCCCTCA 1233
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DB 147152 GATCAAAACATGCTTATGATGATCAACCAAAACAAAGCAATTAATAATGCAAGCCCTCA 147211
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QY 1234 TTGTAGTCTTATGGAATCCCTGCCATCTGATGATGATGATGATGATGATGATGATGAT 1293
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DB 147212 TTGTAGTCTTATGGAATCCCTGCCATCTGATGATGATGATGATGATGATGATGATGAT 147271
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QY 1294 TTGAATCACCTGAGTGAATATTAATTAATTTTCCAGTACAGAAATGTCGTGTGGCC 1353
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DB 147272 TTGAATCACCTGAGTGAATATTAATTAATTTTCCAGTACAGAAATGTCGTGTGGCC 147331
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QY 1354 CATGAAGAACAATAGTATTAAAGATTTTAAAGATTTTAAAGCTCAATTAAGTCT 1413
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DB 147391 CTGTTTGAAGCATGCTCTTAAAGTTTGAATGAACTCAAGACCTTTAGTTCTTTGATC 147450
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DB 147451 CCACTTCACATAGTATGTAATTAATTCGAGCACACCCAGCTCAAAAGACAAACCTCTC 147510
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QY 1534 CTTGCTTAACAGATTAAGTATGATGATCAATCTCAATGCTCTGATTAATAAATGATTAAGGG 1593
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DB 147511 CTTGCTTAACAGATTAAGTATGATGATCAATCTCAATGCTCTGATTAATAAATGATTAAGGG 147570
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QY 1654 A 1654
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Db 147631 A 147631

RESULT 6  
AX709193 1336 bp DNA linear PAT 04-APR-2003

LOCUS  
Sequence 52 from Patent WO02063004.

DEFINITION  
AX709193

ACCESSION  
AX709193.1 GI:29564787

VERSION  
KEYWORDS

SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
1 Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S., Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R., Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H., Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.

TITLE  
G-protein coupled receptors

JOURNAL  
Patent: WO 02063004-A 52.15-AUG-2002;

FEATURES  
source  
1. .1336  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 90012430CB1"

ORIGIN

Query Match 73.0%; Score 1228.6; DB 6; Length 1336;  
Best Local Similarity 99.6%; Pred. No. 2.7e-307;  
Matches 1242; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 29 TCTTTCAGCAATGATTTTCAACATTTATTAATGAAGTTGTAGACTGATTAAGAGATGC 88  
DB 77 TTTTCAGCAATGATTTTCAACATTTATTAATGAAGTTGTAGACTGATTAAGAGATGC 136

QY 89 TCAGCTAAGGAGATTCCTGATGAGCTTTTATGATTAACCAATCCTCTGAAATTCAT 148  
DB 137 TCAGCTAAGGAGATTCCTGATGAGCTTTTATGATTAACCAATCCTCTGAAATTCAT 196

QY 149 GCAAAATGTGACTTCCCAAGTATGCTGGCCACATATCCCGAGAATTCCTTSCGA 208  
DB 197 GCAAAATGTGACTTCCCAAGTATGCTGGCCACATATCCCGAGAATTCCTTSCGA 256

QY 209 TCTATAGTACACCCCACTTAATCAGCTTCTATCTTATAGTGTATTTGGCGGCTGT 268  
DB 257 TCTATAGTACACCCCACTTAATCAGCTTCTATCTTATAGTGTATTTGGCGGCTGT 316

QY 269 GGGGTGATTTCCATTTCTTTTCCCTGCTGGTGAATAACACCGGCTCATGACCAT 328  
DB 317 GGGGTGATTTCCATTTCTTTTCCCTGCTGGTGAATAACACCGGCTCATGACCAT 376

QY 329 GGCGGTATTAATCACTGGTGGTGTGCAAGCGTTTTCTGTCAGTGGCATTTGGCT 388  
DB 377 GGCGGTATTAATCACTGGTGGTGTGCAAGCGTTTTCTGTCAGTGGCATTTGGCT 436

QY 389 GACCTACCTCATCAAGAAGCTTGATGTTGGCTCCCTTCTGCAAAATTTGTAGTGC 448  
DB 437 GACCTACCTCATCAAGAAGCTTGATGTTGGCTCCCTTCTGCAAAATTTGTAGTGC 496

QY 449 CATCTGACATCCACATGTAAGTCTGACGTTCTATTTCTATGTGTGATTCCTGGTACAG 508  
DB 497 CATCTGACATCCACATGTAAGTCTGACGTTCTATTTCTATGTGTGATTCCTGGTACAG 556

QY 509 ATACCTCATCTTCTTCAAGTCAAGAAGCAAGTGAATTCACAGAAATTCGATGCT 568  
DB 557 ATACCTCATCTTCTTCAAGTCAAGAAGCAAGTGAATTCACAGAAATTCGATGCT 616

QY 569 GGCTGCCAGTGTGGCATGTGAGCGTGTGATTTGTCAATGTGTGATCCCTGTGTGTCTC 628

Db 617 GGCTGCCAGTGTGGCATGTGAGCGTGTGATTTGTCAATGTGTGATCCCTGTGTCTC 676

QY 629 CCGGTATGGAATTCATGAGAAATACATAGAGACATCTGTTAAATTTCAAAAAGCT 688  
DB 677 CCGGTATGGAATTCATGAGAAATACATAGAGACATCTGTTAAATTTCAAAAAGCT 736

QY 689 TGCTTACATATGTAAGTAAATCATCACTATATAGTATCATTTTGTATAGCCGTTGC 748  
DB 737 TGCTTACATATGTAAGTAAATCATCACTATATAGTATCATTTTGTATAGCCGTTGC 796

QY 749 TGTGATTCGTGTGCTTCCAGGCTTCATATATATGATGTGACAGCTACGCCA 808  
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QY 809 CTCCTTACATATGTAAGTAAATCATCACTATATAGTATCATTTTGTATAGCCGTTGC 868  
DB 857 CTCCTTACATATGTAAGTAAATCATCACTATATAGTATCATTTTGTATAGCCGTTGC 916

QY 869 CATCTGATTTGTTGCTTCCCTACAGTCTTATAGATCTATATCTTGAATGTGTGAC 928  
DB 917 CATCTGATTTGTTGCTTCCCTACAGTCTTATAGATCTATATCTTGAATGTGTGAC 976

QY 929 GCATTCGAATGCTGTGACAGAGGTTGATTTTAAAGAAATCTTGTAGTGTAC 988  
DB 977 GCATTCGAATGCTGTGACAGAGGTTGATTTTAAAGAAATCTTGTAGTGTAC 1036

QY 989 AGCAATTAATCTGTATGATTTGCTTCTCTTGTGGGGAAGCATTTGTTTAAAGA 1048  
DB 1037 AGCAATTAATCTGTATGATTTGCTTCTCTTGTGGGGAAGCATTTGTTTAAAGA 1096

QY 1049 AAAGATAATTTGGCTTATGGAATTTGTTTGTGCGCTTACCAACAATCTATGATTCAT 1108  
DB 1097 AAAGATAATTTGGCTTATGGAATTTGTTTGTGCGCTTACCAACAATCTATGATTCAT 1156

QY 1109 ATTGCTTCTTATATTTGGGAAT-AAAATGGATATGGGAGATGAATGATTTTCA 1167  
DB 1157 ATTGCTTCTTATATTTGGGAAT-AAAATGGATATGGGAGATGAATGATTTTCA 1216

QY 1168 TTACTTGATCAAAACCATGCTTGTATGATCCCAAAACCAAGATTAATTAATGCAAG 1227  
DB 1217 TTACTTGATCAAAACCATGCTTGTATGATCCCAAAACCAAGATTAATTAATGCAAG 1276

QY 1228 CCTCATTTAGTCTTATGGAATCCCTCCATCTCTGATGATGCG 1274  
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RESULT 7  
AX709194 1340 bp DNA linear PAT 04-APR-2003

LOCUS  
Sequence 53 from Patent WO02063004.

DEFINITION  
AX709194

ACCESSION  
AX709194.1 GI:29564788

VERSION  
KEYWORDS

SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
1 Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S., Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R., Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H., Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.

TITLE  
G-protein coupled receptors

JOURNAL  
Patent: WO 02063004-A 53.15-AUG-2002;

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"  
/note="Incyte ID No: 90012586CB1"

ORIGIN

Query Match 65.7%; Score 1106.2; DB 6; Length 1340;  
Best Local Similarity 99.6%; Pred. No. 1.5e-275;  
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 153 AATGAGCTTCCCAAGTATGCTGCGCCACATACCTCCAGAAATTCCTCTGGAGTCT 212  
DB 205 ACAGGTGACTTCCCAAGTATGCTGCGCCACATACCTCCAGAAATTCCTCTGGAGTCT 264  
QY 213 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTATTTGGCGGCTGGT 272  
DB 265 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTATTTGGCGGCTGGT 324  
QY 273 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 332  
DB 325 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 384  
QY 333 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 392  
DB 385 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 444  
QY 393 TACCTCATCAAGAAAGACTTGGATTTGGGCTGCCCTTTCGCAAAATTTGTAAGTCCATG 452  
DB 445 TACCTCATCAAGAAAGACTTGGATTTGGGCTGCCCTTTCGCAAAATTTGTAAGTCCATG 504  
QY 453 CTGCACATCCACATGTACCTCAACGTTCTTATTTAGTGGATCTGTGACCAAGATAC 512  
DB 505 CTGCACATCCACATGTACCTCAACGTTCTTATTTAGTGGATCTGTGACCAAGATAC 564  
QY 513 CTGATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATTCGATGCTGGCT 572  
DB 565 CTGATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATTCGATGCTGGCT 624  
QY 573 GCCAGTCTGGCATGTGGAAGCGCTGTGATTTGTCTTGTGTAACCCCTGGTGTCTCCCG 632  
DB 625 GCCAGTCTGGCATGTGGAAGCGCTGTGATTTGTCTTGTGTAACCCCTGGTGTCTCCCG 684  
QY 633 TATGGAATCCATGAGAAATCAATGAGAGACAGTCTTAAATTTTCAAAAGAGCTTGCCT 692  
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QY 693 TACACATATGTGAATAATCATCACTATATGATGATCTTTTGTCTAGTCCGCTGTGTG 752  
DB 745 TACACATATGTGAATAATCATCACTATATGATGATCTTTTGTCTAGTCCGCTGTGTG 804  
QY 753 ATTCTGTGGTCTTCCAGGTCCTTCACTATATGATGATGATGATGATGATGATGATGAT 812  
DB 805 ATTCTGTGGTCTTCCAGGTCCTTCACTATATGATGATGATGATGATGATGATGATGAT 864  
QY 813 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAAACGATATTTTATAGGGGCTGATC 872  
DB 865 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAAACGATATTTTATAGGGGCTGATC 924  
QY 873 CTGTGTGTGTCTTCCCTACAGTCTTATAGATCTATTAATCTGAAATGTTGTGACGAT 932  
DB 925 CTGTGTGTGTCTTCCCTACAGTCTTATAGATCTATTAATCTGAAATGTTGTGACGAT 984  
QY 933 TCCAAATGCTGTAGACAGAAAGTTCATTTTATAGAAATCTTCTGAGTGTACGCA 992  
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QY 993 ATTAGCTGTATGATTTGCTTCTTGTGCTTTGGGGAAAGCCATTTGTTAAAGCAAG 1052  
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QY 1053 ATTAATGGCTTATGAAATTTGTTTGTGCGTGTAGCCAAATCTACAGATTCATATTT 1112  
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QY 1113 GCTTCTTTATATTTGGGAAT-AAAAATGGGATATAGGGAGGTAAAGATGATTTTCATTAAC 1171

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DB 1225 TTGATCAAAAACATGCTGCTGATGTACCCAAACAAAGAGACTTAATAATGCAAGCCCT 1284  
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DB 1285 CATTGATGCTCTTATGAGATCCCTCCCATCTCTGAGTATGCG 1327

RESULT 8  
AX709195 1460 bp DNA linear PAT 04-APR-2003  
LOCUS Sequence 54 from Patent WO02063004.  
DEFINITION AX709195  
ACCESSION AX709195  
VERSION AX709195.1 GI:29564789  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Baughn, M.R., Tibbuley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kalliock, D.A., Gandhi, A.R., Walla, N.K., Ariz, C., Elliott, V.S.,  
Hafalla, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Grail, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,  
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
Harland, L.  
G-protein coupled receptors  
Patent: WO 02063004-A 54 15-AUG-2002;  
JOURNAL Incyte Genomics, Inc. (US)  
FEATURES  
source  
1. 1460  
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/note="Incyte ID No: 90012670CB1"

ORIGIN

Query Match 65.7%; Score 1106.2; DB 6; Length 1460;  
Best Local Similarity 99.6%; Pred. No. 1.5e-275;  
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 153 AATGAGCTTCCCAAGTATGCTGCGCCACATACCTCCAGAAATTCCTCTGGAGTCT 212  
DB 325 ACAGGTGACTTCCCAAGTATGCTGCGCCACATACCTCCAGAAATTCCTCTGGAGTCT 384  
QY 213 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTATTTGGCGGCTGGT 272  
DB 385 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTATTTGGCGGCTGGT 444  
QY 273 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 332  
DB 445 GTCAATTCATATCTTTCTCTCTGCTGTAAGAAACACCGGTCAGTACCAACCATGGC 504  
QY 453 CTGCACATCCACATGTACCTCAACGTTCTTATTTAGTGGATCTGTGACCAAGATAC 512  
DB 505 CTGCACATCCACATGTACCTCAACGTTCTTATTTAGTGGATCTGTGACCAAGATAC 564  
QY 513 CTGATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATTCGATGCTGGCT 572  
DB 685 CTGATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATTCGATGCTGGCT 744

QY	573	GCAGATGCTGGCAATTTGGACCGCTGGTGAATTTGTCATTTGGTGTACCCCTGGTGTCTTCCCGG	632
Db	745	GCAGATGCTGGCAATTTGGACCGCTGGTGAATTTGTCATTTGGTGTACCCCTGGTGTCTTCCCGG	804
QY	633	TATGAAATCCCAATGAGAATATACAAATAGAGACACTGTGTTTAAATTTCAAAAAGAGCTTCT	692
Db	805	TATGAAATCCCAATGAGAATATACAAATAGAGACACTGTGTTTAAATTTCAAAAAGAGCTTCT	864
QY	633	TACACAAATGTGAAAAATCATCAACTATAATGATGATCATTTTGTCTATGACCGTGTCTGTG	752
Db	865	TACACAAATGTGAAAAATCATCAACTATAATGATGATCATTTTGTCTATGACCGTGTCTGTG	924
QY	753	ATTTCGTTGGTCTTCCAGGTCTTCACTCATATATGTGATGGTGCAGAACTACGCCACTCT	812
Db	925	ATTTCGTTGGTCTTCCAGGTCTTCACTCATATATGTGATGGTGCAGAACTACGCCACTCT	984
QY	813	TTACTATCCCAACAGAGGTTCTGGGCTCAGCTGAAAAAACCTAATTTTATATGGGGTCTATC	872
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QY	873	CTGTGTTGTTTCCCTTCCCTACAGTCTTTAAGATCTATTACTTGAATGTTGTGACGCAT	932
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QY	933	TTCCATAGGCTGTAGAGACAGAGTTCATTTTATATACGAAATCTTCTTAGTGTATACAGA	992
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QY	993	ATTAGCTGCTATGATTTTGTCTCTCTTGTGCTTTGGGGGAGAGCAATGGTTTATAGCAAAAG	1052
Db	1165	ATTAGCTGCTATGATTTTGTCTCTCTTGTGCTTTGGGGGAGAGCAATGGTTTATAGCAAAAG	1224
QY	1053	ATPAATGGCTTATGGAAATGTGTTTGTGCCGTATAGCCAAACATACAGTATTCATATTT	1112
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QY	1113	GCTTCTCTTATATATTTGGGAAT-AAATAGGCTATAGGGAGGTTAAGATGTTATTTCAATTAC	1170
Db	1285	GCTTCTCTTATATATTTGGGAATAAATATGGGCTATAGGGAGGTTAAGATGTTATTTCAATTAC	1344
QY	1172	TTGATCAAAAACATGCTCTTGATGTATGCCAAAACAAAAGAGCATATPAATATGACAGAGCCCT	1231
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QY	1232	CATTGTAGTCTTATNGGATCCCTCCCATCTCTGATGATGAGC 1274	
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LOCUS	AX451925		linear
DEFINITION	Sequence 22 from Patent WO022825.		
ACCESSION	AX451925		
KEYWORDS	AX451925.1 GI:21698748		
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Baughn, M.R., Graul, R.C., Wala, N.K., Gandhi, A.R., Hafalia, A.J.,		
	Rankumar, J., Tribouley, C.M., Thornton, M., Kallick, D.A., Yao, M.G.,		
	Ellicott, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,		
	Roopa, R., Nguyen, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and		
	Policky, J.L.		
TITLE	G-protein coupled receptors		
JOURNAL	Patent: WO 0226825-A 22 04-APR-2002;		
FEATURES	Incyte Genomics, Inc. (US)		
	Location/Qualifiers		
SOURCE	1. 1499		
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ORIGIN	/db_xref="taxon:9606" /note="Incyle ID No: 6157025CBI"				
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Matches 1091;	Conservative	0;	Mismatches 10;	Indels 5;	Gaps 5
QY	157	GTGACTTCCCAAGTATGCTGCGCCACATATACCTCCAGGAATTCCTCTTGCAATCCTATAG	216		
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QY	217	TGACACCCCACTTAATCAAGCCTCTAATCTTCAATAGTGTCTTATTTGGGGGGCTGTGGGTGTCA	276		
Db	427	TGACACCCCACTTAATCAAGCCTCTAATCTTCAATAGTGTCTTATTTGGGGGGCTGTGGGTGTCA	486		
QY	277	TTTGCAATCTTTTCTCTCGTGGTGAAGAAACACCCGGTCAAGTACCAACATGGCGGTCA	336		
Db	487	TTTGCAATCTTTTCTCTCGTGGTGAAGAAACACCCGGTCAAGTACCAACATGGCGGTCA	546		
QY	337	TTAACTTGGTGGTGTCCACAGCGTTTTTCTGTGACAGTGCATTTTGCTTGAACCTTACC	396		
Db	547	TTAACTTGGTGGTGTCCACAGCGTTTTTCTGTGACAGTGCATTTTGCTTGAACCTTACC	606		
QY	397	TCATCAAGAGAATCTTGATGTTTGGGGCTGCCCTTCTGCAATTTTGTAGTGCATGTGCG	456		
Db	607	TCATCAAGAGAATCTTGATGTTTGGGGCTGCCCTTCTGCAATTTTGTAGTGCATGTGCG	666		
QY	457	ACATCAACATGACCTCAACGTTCCTATCTATATGTGGATATCTGGTCAACAGATPACCTCA	516		
Db	667	ACATCAACATGACCTCAACGTTCCTATCTATATGTGGATATCTGGTCAACAGATPACCTCA	726		
QY	517	TCTTCTTCAAGTGCAGAAACAAAGTGTGAATCTTACAGAAACCTGCATGCTGTGGCTGCC	576		
Db	727	TCTTCTTCAAGTGCAGAAACAAAGTGTGAATCTTACAGAAACCTGCATGCTGTGGCTGCC	786		
QY	577	GTGCTGCGATGTGACGCTGGTGAATGTGCATTTGTGTGTACCCCTGGTGTCTCCGGTATG	636		
Db	787	GTGCTGCGATGTGACGCTGGTGAATGTGCATTTGTGTGTACCCCTGGTGTCTCCGGTATG	846		
QY	637	GAATCCATGAGGAATPACATATAGAGACCTGTTTAAATTTTACAAAGAGCTTGCTTAC	696		
Db	847	GAATCCATGAGGAATPACATATAGAGACCTGTTTAAATTTTACAAAGAGCTTGCTTAC	906		
QY	697	CATATGTGAATCATCACTATATATAGATGATCATTTTGTGATAGCGTTGCTGTGATTC	756		
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QY	757	TGTTGGTCTTCCAGGTCTTCATCATATATATGTGATGTGCAGAGCTACGCCACTCTTTAC	816		
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QY	817	TATCCCAACAGAGATTTCTGGGCTCAAGCTGAAACCTATTTTTTATATAGGGTCAATCCTTG	876		
Db	1027	TATCCCAACAGAGATTTCTGGGCTCAAGCTGAAACCTATTTTTTATATAGGGTCAATCCTTG	1086		
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QY	937	ATGCCCTGAGCAGAAAGGTGTCATTTTATACGAATCTTCTTGAAGTATACAGCAATTA	996		
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Qy 1176 TCAAAACATGCGCTTGAATGATGCCAAAACAAAAGAGATCTAAATGCAAGAGCCCTCATTT 1235  
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Db 1443 GTAGTCTTATGGGATGCCCTCCCATTC 1468  
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RESULT 10  
AX453412 1051 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 1 from Patent WO0244212.  
DEFINITION AX453412  
VERSION AX453412.1 GI:21712725  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Deleersnijder, W., Blockx, H. and de Moor, L.  
TITLE Human g-protein coupled receptor and uses thereof  
JOURNAL Patent: WO 0244212-A 1 06-JUN-2002;  
SOLVAY PHARMACEUTICALS B V (NL)  
FEATURES  
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ORIGIN  
Query Match 58.9%; Score 991.2; DB 6; Length 1051;  
Best Local Similarity 99.6%; Pred. No. 9.8e-246;  
Matches 1004; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
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Db 104 AGTGAACCCCACTTATAGCCCTCTCATGTGCTTATTTGCGGGCGGTGGGGTGT 163  
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LOCUS Sequence 23829 from Patent WO02068579.  
DEFINITION CQ737895  
VERSION CQ737895.1 GI:42337355  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanecons or transcripts, for detecting expression and other uses  
theroeof  
JOURNAL Patent: WO 02068579-A 23829 06-SEP-2002;  
PE Corporation (NY) (US)  
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Best Local Similarity 99.9%; Pred. No. 5.8e-230;

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Qy	277	TTTTCATCTTTTCTCTCTGTGAAATGAACACCCGGTGAATGACCAATGGCGGTCA	336						
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Qy	337	TTTACCTGGTGGTGCACAGGGTTTTTCTGCTGACAGTGCATTTGGCTGACCTACC	396						
Db	581	TTTACCTGGTGGTGCACAGGGTTTTTCTGCTGACAGTGCATTTGGCTGACCTACC	640						
Qy	397	TCAATCAAGAACTTGGATGTTGGGCTGCCTCTGCAATTTGTGATGCCATGCTGC	456						
Db	641	TCAATCAAGAACTTGGATGTTGGGCTGCCTCTGCAATTTGTGATGCCATGCTGC	700						
Qy	457	ACATCCACATGATCTCACTTCTATTTCTATGTGTGATCTGTGACCAATATCTCA	516						
Db	701	ACATCCACATGATCTCACTTCTATTTCTATGTGTGATCTGTGACCAATATCTCA	760						
Qy	517	TCCTCTCAAGTGAAGAAAGATGGAATTTCTACAGAAATGCAATGCTGTGGCTGCCA	576						
Db	761	TCCTCTCAAGTGAAGAAAGATGGAATTTCTACAGAAATGCAATGCTGTGGCTGCCA	820						
Qy	577	GTGCTGACATGATGACGCTGTGATTTGTCAATGTGTATCCCTGTGTCTCCCGATAG	636						
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Qy	637	GAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCAACAAAGCTTGTCTTACA	696						
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Qy	697	CATATGGAATCATCATATATATATATGATGATTTTGTATAGCCGTGTGTGATTC	756						
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Qy	757	TGTTGTCTTCAAGCTTCTATATATATATATATATATATATATATATATATATATAT	816						
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RESULT 12  
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LOCUS  
DEFINITION Novel Polypeptide.  
ACCESSION BD187510  
VERSION BD187510.1 GI:32997249

KEYWORDS JP 2003024082-A/1.									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS Lee, H.									
TITLE Novel Polypeptide									
JOURNAL Patent: JP 2003024082-A 1 28-JAN-2003;									
COMMENT Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)									
OS Homo sapiens									
PN JP 2003024082-A/1									
PD 28-JAN-2003									
PF 17-JAN-2002 JP 2002008881									
PI 23-JAN-2001 GB 0101739.1									
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Best Local Similarity 99.9%; Pred. No. 2.4e-226;									
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	171	ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCCTATATAGTGAACCCCACTTA	230						
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Qy	351	GTCCACAGGTTTTTCTGCTGACAGTGCATTTGCTTACCTTACCTCATCAAGAGACT	410						
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Qy	411	TGATATTTGGGCTGCTTCTGCAATTTTGAATGTCATGTGCAATCCATGATTC	470						
Db	241	TGATATTTGGGCTGCTTCTGCAATTTTGAATGTCATGTGCAATCCATGATTC	300						
Qy	471	CTCAGTCTCTATTTCAATGATGATCCCTGTCACCGATACCTCATCTTCTTCAAGTGC	530						
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Qy	591	ACGCTGTATTTGTCTTTGTGTAACCTGTTGTCTCCCGTATGGAATCCATGAGAA	650						
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RESULT 13  
AX481576 918 bp DNA linear PAT 16-AUG-2002  
LOCUS AX481576  
DEFINITION Sequence 1 from Patent EP1225183.  
ACCESSION AX481576  
VERSION AX481576.1 GI:22316490  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Harland, L.  
TITLE Human g-protein coupled receptor  
JOURNAL Patent: EP 1225183-A 1 24-JUL-2002;  
Pfizer Limited (GB); PFIZER INC. (US)  
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Best Local Similarity 99.9%; Pred. No. 2.4e-226;  
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QY 171 ATGCTGGCCCAATACCTCCAGGAATTCCTTGGCATCCTATAGTACACCCCACTTA 230  
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RESULT 14  
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LOCUS AX498180  
DEFINITION Sequence 3 from Patent WO242461.  
ACCESSION AX498180  
VERSION AX498180.1 GI:23343111  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.  
TITLE Endogenous and non-endogenous versions of human g protein-coupled  
JOURNAL receptors  
PATENT: WO 0242461-A 3 30-MAY-2002;  
Arenas Pharmaceuticals, Inc. (US)  
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Query Match 54.4%; Score 916.4; DB 6; Length 918;  
Best Local Similarity 99.9%; Pred. No. 2.4e-226;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 171 ATGCTGGCCCAATACCTCCAGGAATTCCTTGGCATCCTATAGTACACCCCACTTA 230  
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Qy 411 TGAATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATGCTGACATCCATGATAC 470
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Qy 591 ACCGTGTGATGTGCATGTGTGTAACCCCTGCTGTCTCCGGTATGGAATCCATGAGAA 650
Db 421 ACCGTGTGATGTGCATGTGTGTACCCCTGCTGTCTCCGGTATGGAATCCATGAGAA 480
Qy 651 TACAAATGAGAGCATCTTTTAAATTTACAAAGAGCTTCTTACATATGTGAAATC 710
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Qy 1071 TGTGTTTGTGCCCTTAG 1088
Db 901 TGTGTTTGTGCCCTTAG 918

RESULT 15
BD105324 918 bp DNA linear PAT 27-AUG-2002
LOCUS Novel G protein-coupled receptor protein and its DNA.
DEFINITION
ACCESSION BD105324.1 GI:22650898
VERSION WO 0196567-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 918)
Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.
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TITLE Novel G protein-coupled receptor protein and its DNA
JOURNAL Patent: WO 0196567-A 1 20-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
COMMENT WO 0196567-A/1
PD 20-DEC-2001
PE 14-JUN-2001 WO 2001JP005061
PR 15-JUN-2000 JP 00P 184596.19-JUL-2000 JP 00P 223887.PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00,
PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC
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CC Novel G protein-coupled receptor protein and its DNA FH Key
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FEATURES
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ORIGIN
Query Match 54.4%; Score 916.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 2,4e-226;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 171 ATGCTGGGCACAAATCTCTCAGAGAAATCTCTTGGATCTTATGACACCCCACTTA 220
Db 1 ATGCTGGGCACAAATCTCTCAGAGAAATCTCTTGGATCTTATGACACCCCACTTA 60
Qy 231 ATGAGCCTACTCTCATAGTGCCTTATGGCGGGCTGTGGGTGCATTTCCATCTTTTC 290
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Db 661 TTCTGGGCTCAGCTGAATAACCTATTTTATPAGGGGTCACTTGTGTTCTCTCC 720
Qy 891 TACCAATTCTTTAGATCTATTAATGTAATGTTGACGCAATCCCAATGCCGTAGCAGC 950
Db 721 TACCAATTCTTTAGATCTATTAATGTAATGTTGACGCAATCCCAATGCCGTAGCAGC 780
Qy 951 AAGGTGATTTTATTAAGAAATCTTCTGAGTGAACAGCAATTAGCTGATGATTTG 1010
Db 781 AAGGTGATTTTATTAAGAAATCTTCTGAGTGAACAGCAATTAGCTGATGATTTG 840
Qy 1011 CTTCCTTTGCTTTGGGGGAAGCCATTGTTTAAAGCAAAAGATATTGGCTATGGAAT 1070
Db 841 CTTCCTTTGCTTTGGGGGAAGCCATTGTTTAAAGCAAAAGATATTGGCTATGGAAT 900
Qy 1071 TGTGTTTGTGCCGTTAG 1088
Db 901 TGTGTTTGTGCCGTTAG 918
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Search completed: September 10, 2005, 07:21:29  
Job time : 7576.62 secs

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XX 01-MAR-2001; 2001US-0272677P.  
PR (MILL-) MILLENNIUM PHARM INC.  
PA Glucksmann MA;  
XX WPI; 2002-732793/79.  
DR P-PDSB; MA022919.  
XX  
FT New G-protein coupled receptor used in receptor assays as a target for  
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
PT disorders.  
PS Claim 5; Page 99-100; 105pp; English.  
XX  
CC The invention relates to an isolated polypeptide, which is a G-protein  
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
CC receptor type proteins (GPCRs), designated the 93870 receptor. The  
CC polypeptides, nucleic acid molecules and antibodies of the invention are  
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
CC monitoring clinical trials or pharmacogenetics), or in methods of  
CC treatment (e.g. therapeutic and prophylactic). They are useful in  
CC treating and diagnosing conditions related to aberrant activity or  
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
CC disorders, or bone marrow mononuclear disorders, as well as cellular  
CC proliferative and/or differentiative disorders, hormonal disorders,  
CC neurological disorders, cardiovascular disorders, viral diseases, liver  
CC disorders, and pain and metabolic disorders. Conditions that can be  
CC treated include cancer, diabetes mellitus, hypothyroidism,  
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or  
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,  
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,  
CC Huntington's disease, heart failure, angina pectoris, myocardial  
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
CC transgenic animals are useful for studying the function and/or activity  
CC of a 93870 protein and for identifying and/or evaluating modulators of  
CC 93870 activities. The polynucleotides of the invention can be used in  
CC gene therapy. This polynucleotide sequence represents the cDNA of the  
CC 1684 nucleotide human G-protein coupled receptor type protein of the  
CC invention  
XX  
SQ Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;  
Query Match 99.9%; Score 1683; DB 6; Length 1684;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCGACAGGTGACACAAATTTTCCAACTATCTTTAGCAATGATTTTCAACAATTATATAAA 60  
DB 1 TCGACAGGTGACACAAATTTTCCAACTATCTTTAGCAATGATTTTCAACAATTATATAAA 60  
QY 61 TGGAGTTGTAGATCGATAGAGATGCTCACTAAGGAGATCTCTGATGCGCTTTAGA 120  
DB 61 TGGAGTTGTAGATCGATAGAGATGCTCACTAAGGAGATCTCTGATGCGCTTTAGA 120  
QY 121 TTGATACACCAATCTCTGAATTCATGCAAAAATGTGACTTCCCAAGTAGCTGGCC 180  
DB 121 TTGATACACCAATCTCTGAATTCATGCAAAAATGTGACTTCCCAAGTAGCTGGCC 180  
QY 181 ACAATACCTCGAGAAATTCCTTGGCATCTTAAGTACACCCCACTTAATCAGCCCTT 240  
DB 181 ACAATACCTCGAGAAATTCCTTGGCATCTTAAGTACACCCCACTTAATCAGCCCTT 240  
QY 241 ACTTCATAGTGTATTTGGCGGCGCTGTGGGTGATTTCCATTTCTTCTCTGGTGA 300  
DB 241 ACTTCATAGTGTATTTGGCGGCGCTGTGGGTGATTTCCATTTCTTCTCTGGTGA 300  
QY 301 AATGAAACCCGGTCAGTGACCAACATGCGGTGATTAATCTGGTGTGTCACAGCG 360

DB 301 AATGAAACCCGGTCAGTGACCAACATGCGGTGATTAATCTGGTGTGTCACAGCG 360  
QY 361 TTTTTCGTGAGAGGCCATTTTCGCTTGAACCTCACTCAAGAGACTTGGATGTTGG 420  
DB 361 TTTTTCGTGAGAGGCCATTTTCGCTTGAACCTCACTCAAGAGACTTGGATGTTGG 420  
QY 421 GGCCTGCCCTCTGCAATTTGTAGTGCCATGCTGACATCCACATGATACCTTCC 480  
DB 421 GGCCTGCCCTCTGCAATTTGTAGTGCCATGCTGACATCCACATGATACCTTCC 480  
QY 481 TATTCATAGTGTATCTGCTGTCACAGATACCTCATCTTCTCAAGTGAAGACAAAG 540  
DB 481 TATTCATAGTGTATCTGCTGTCACAGATACCTCATCTTCTCAAGTGAAGACAAAG 540  
QY 541 TGGATATTCACAAAACTGCATGCTGTGCTGCCATGCTGTCAGATGTCAGCTGTGA 600  
DB 541 TGGATATTCACAAAACTGCATGCTGTGCTGCCATGCTGTCAGATGTCAGCTGTGA 600  
QY 601 TTGTCATTTGTATACCCCTGTTGTCTCCCGGTATGGAATTCATGAGAAATCAATGAG 660  
DB 601 TTGTCATTTGTATACCCCTGTTGTCTCCCGGTATGGAATTCATGAGAAATCAATGAG 660  
QY 661 AGCACTGTTTAAATTTCAAAAGAGCTTGTACATATGTGAAATTCATCACTATA 720  
DB 661 AGCACTGTTTAAATTTCAAAAGAGCTTGTACATATGTGAAATTCATCACTATA 720  
QY 721 TGATAGTCATTTTGTATAGCCGCTGTGTATTTCTGTGTGCTTCCAGTCTTATCA 780  
DB 721 TGATAGTCATTTTGTATAGCCGCTGTGTATTTCTGTGTGCTTCCAGTCTTATCA 780  
QY 781 TTATGTGATAGTGAGCAAGACTACGCACTCTTACTATCCACAGAGTTTGAGGCTC 840  
DB 781 TTATGTGATAGTGAGCAAGACTACGCACTCTTACTATCCACAGAGTTTGAGGCTC 840  
QY 841 AGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTCTTCCCTACCAAGTCT 900  
DB 841 AGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTCTTCCCTACCAAGTCT 900  
QY 901 TTGAGATCTTATCTTGAATGTTGTGACAGATTCCAATGCTGTACAGAGAGTTGCAT 960  
DB 901 TTGAGATCTTATCTTGAATGTTGTGACAGATTCCAATGCTGTACAGAGAGTTGCAT 960  
QY 961 TTTATATGAAATCTTCTGAGTGATAACAGATTAAGCTGTGATTTGCTCTCTTG 1020  
DB 961 TTTATATGAAATCTTCTGAGTGATAACAGATTAAGCTGTGATTTGCTCTCTTG 1020  
QY 1021 TCTTTGGGGAGAGCCATTTGTTAAGCAAAAGATTAATGCTTATGGAATTTGTTTGT 1080  
DB 1021 TCTTTGGGGAGAGCCATTTGTTAAGCAAAAGATTAATGCTTATGGAATTTGTTTGT 1080  
QY 1081 GCGGTATGCCAACAATCTAGATATCTATTTGCTCTTATATTTGGGAAATTAATGGG 1140  
DB 1081 GCGGTATGCCAACAATCTAGATATCTATTTGCTCTTATATTTGGGAAATTAATGGG 1140  
QY 1141 TATAGGGAGAGTAAGATGATATTTCACTAATCTGATCAAAACCATGCTTATGTAACCA 1200  
DB 1141 TATAGGGAGAGTAAGATGATATTTCACTAATCTGATCAAAACCATGCTTATGTAACCA 1200  
QY 1201 AAACAAAAGACTATAAATGCAAGAGCCCTCATTTGATCTTATGGAATTCCTCCAT 1260  
DB 1201 AAACAAAAGACTATAAATGCAAGAGCCCTCATTTGATCTTATGGAATTCCTCCAT 1260  
QY 1261 CTCTGAGTATGCGCGGTACAAAGACAGATTTGTGTAATCCACCTGAGTTGCAATTTA 1320  
DB 1261 CTCTGAGTATGCGCGGTACAAAGACAGATTTGTGTAATCCACCTGAGTTGCAATTTA 1320  
QY 1321 CATTAATTTCCAGTACGAATGCTGTGTGCGCCATGAAAGCAACATAGGTTTAAAGT 1380  
DB 1321 CATTAATTTCCAGTACGAATGCTGTGTGCGCCATGAAAGCAACATAGGTTTAAAGT 1380  
QY 1381 TTTNAGATTTCAATTAGCTCATTTAAGTTCTCTGTTTGAACATAGTCTCTTAAGTTT 1440



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Db 549 TACACATATGGAATATCATCACTATATGATGATCTTTTGTCTAGAGCGTTGCTGTG 608
Qy 753 ATTCTGTGGTCTTCCAGGCTTTCATCATATATGTTGATGCGAAGCTACGCCACTCT 812
Db 609 ATTCTGTGGTCTTCCAGGCTTTCATCATATATGTTGATGCGAAGCTACGCCACTCT 668
Qy 813 TTACTATCCACGAGAGTTCTGGGCTCAGCTGAAAAACCATTTTATAGGGGCTATC 872
Db 669 TTACTATCCACGAGAGTTCTGGGCTCAGCTGAAAAACCATTTTATAGGGGCTATC 728
Qy 873 CTGTGTTGTTCCCTTCCCTACAGCTCTTTAGATCTATTAATTGAATGTTGTGACGCAT 932
Db 729 CTGTGTTGTTCCCTTCCCTACAGCTCTTTAGATCTATTAATTGAATGTTGTGACGCAT 788
Qy 933 TCCATATGCTGTACAGACAGAGTTGCATTTTATATACGAATCTTCTGAGTGTACAGCA 992
Db 789 TCCATATGCTGTATACAGACAGAGTTGCATTTTATATACGAATCTTCTGAGTGTACAGCA 848
Qy 993 ATTAGCTGTATGATTTGCTCTCTTGTGCTTTGCGGGGAGAGCATTTGGTTTAAAGCAAA 1052
Db 849 ATTAGCTGTATGATTTGCTCTCTTGTGCTTTGCGGGGAGAGCATTTGGTTTAAAGCAAA 908
Qy 1053 ATAAATGGCTTATGGAATGTGTTTGTGCGGTTAGCCACAACTACAGATTTGATATT 1112
Db 909 ATAAATGGCTTATGGAATGTGTTTGTGCGGTTAGCCACAACTACAGATTTGATATT 968
Qy 1113 GCTTCCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGGTATTTGATTAAC 1171
Db 969 GCTTCCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGGTATTTGATTAAC 1028
Qy 1172 TTGATCAAAAACCATGCTTGTATGTACCCAAAACAAAAGACCTATTAATGCAAGAGCCCT 1231
Db 1029 TTGATCAAAAACCATGCTTGTATGTACCCAAAACAAAAGACCTATTAATGCAAGAGCCCT 1088
Qy 1232 CATTGTAGTCCCTTATGGAGTCCCTCCCATCTGTAGTGTAGTGGCGGTACAAAGACAGTGT 1291
Db 1089 CATTGTAGTCCCTTATGGAGTCCCTCCCATCTGTAGTGTAGTGGCGGTACAAAGACAGTGT 1148
Qy 1292 TGTGTAATCCACCTGAGGTGCAATATTAATTTTCCAGTACAGAAATGTCTGTGTGG 1351
Db 1149 TGTGTAATCCACCTGAGGTGCAATATTAATTTTCCAGTACAGAAATGTCTGTGTGG 1208
Qy 1352 CCCATGAAGAACAATAGTGTATTAAGATTTTAAAGATTTTCAATAGGCTCATTTCAAGTTC 1411
Db 1209 CCCATGAAGAACAATAGTGTATTAAGATTTTAAAGATTTT-AGAGTTTATTAAGCTCATTTCAAGTTC 1267
Qy 1412 CTCTGTGTTGAAGCATGTCTCTTAAGTTTTGGAGTGAACCTGACACTTTAGTCTTTTCA 1471
Db 1268 CTCTGTGTTGAAGCATGTCTCTTAAGTTTTGGAGTGAACCTGACACTTTAGTCTTTTCA 1327
Qy 1472 TCCCACTTCAACATAGTAAATTAATCTGGCCACACCCGAGCTCCAAAGACAAATCTC 1531
Db 1328 TCCCACTTCAACATAGTAAATTAATCTGGCCACACCCGAGCTCCAAAGACAAATCTC 1387
Qy 1532 TCCTTGTGTAACAGGTAGATGTCCCATTCATCTCATGATGCTGATTAATAAAGCTGATAAG 1591
Db 1388 TCCTTGTGTAACAGGTAGATGTCCCATTCATCTCATGATGCTGATTAATAAAGCTGATAAG 1447
Qy 1592 GGAAGAAATAGTAAAAATTTTCTAGGGTATCAATTAACCTGTGTAAGAAAGTCAATCTGTCT 1651
Db 1448 GGAAGAAATAGTAAAAATTTTCTAGGGTATCAATTAACCTGTGTAAGAAAGTCAATCTGTCT 1507
Qy 1652 AGA 1654
Db 1508 AGA 1510
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## RESULT 3

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ABST0242 ID ABST0242 standard; DNA; 2525 BP.
XX AC ABST0242;
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XX 26-NOV-2002 (first entry)
DT XX
XX DNA encoding human G protein-coupled receptor, nGPR-16.
DE XX
XX Human; gene; de; G protein-coupled receptor; GPCR; nGPR; beGPR;
KM nG protein coupled receptor; communication; serpentine structure;
KM seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KM genetic predisposition; brain; immune response; gene therapy;
KM anxiety disorder; depression; bipolar disorder; schizophrenia;
KM Huntington's disease; dyskinesia; manic depression; stroke;
KM Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KM tranquiliser.
XX
OS Homo sapiens.
XX
XX W0200264789-A1.
FN
XX
XX 22-AUG-2002.
PD
XX
XX 14-FEB-2001; 2001MO-US004641.
PF
XX
XX 14-FEB-2001; 2001MO-US004641.
PR
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
PA
XX
XX Lind P, Parodi LA, Vogel G, Wood LS;
PI
XX WPI, 2002-674879/72.
DR
XX P-PSDB; ABG93787.
XX
XX New nucleic acids and polypeptides of the nG protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
XX Example 1; Page 84-85; 244pp; English.
PS
XX
XX The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC nG protein coupled receptor-14 (nGPR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nGPR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder
CC and for identifying a compound useful as a modulator of binding between
CC nGPR-14 and a binding partner of nGPR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesia, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABST0202-ABST0248, ABST0338 and ABST0243 are the DNAs
CC encoding the nGPRs (also referred to as beGPCRs)
XX
SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;
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Query Match 87.4%; Score 1472.6; DB 6; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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```
Qy 153 AATGTACTTCCCAAGTATGCTGCGCACAAATCTCCAGAAATCTCTTGGAGATCT 212
Db 9 ACAAGTACCTTCCCAAGTATGCTGCGCACAAATCTCCAGAAATCTCTTGGAGATCT 68
```

OY	213	ATATGACACCCCACTTAATCAAGCCTCTACTATATAGTGGCTTAATGGCGGGCTGGTGGGT	272
Db	69	ATATGACACCCCACTTAATCAAGCCTCTACTATATAGTGGCTTAATGGCGGGCTGGTGGGT	128
OY	273	GTCAATTCATCTTCTTCTCCGGGAAATGAACACCGGGTCAAGTGCACCAATGGG	332
Db	129	GTCAATTCATCTTCTTCTCCGGGAAATGAACACCGGGTCAAGTGCACCAATGGG	188
OY	333	GTCAATTCATCTTCTTCTCCGGGAAATGAACACCGGGTCAAGTGCACCAATGGG	392
Db	189	GTCAATTCATCTTCTTCTCCGGGAAATGAACACCGGGTCAAGTGCACCAATGGG	248
OY	393	TACCTCATCAAGAAGACTTGATGTTTGGGCTGCCCTTTCGCAAAATTTGTAGTGCATG	452
Db	249	TACCTCATCAAGAAGACTTGATGTTTGGGCTGCCCTTTCGCAAAATTTGTAGTGCATG	308
OY	453	CTGCACATCCACATGATGACCTCAGTTCCTCAATCTATGAGGATCCTGGTCAACGATAC	512
Db	309	CTGCACATCCACATGATGACCTCAGTTCCTCAATCTATGAGGATCCTGGTCAACGATAC	368
OY	513	CTCATCTCTTTCAGAGTGCAGAAACAAAGTGAATTTACAGAAAACTGCATCTGTGGT	572
Db	369	CTCATCTCTTTCAGAGTGCAGAAACAAAGTGAATTTACAGAAAACTGCATCTGTGGT	428
OY	573	GCGAGTGTGGGATGTGACGCTGGTGAATGTTCATTTGTGTGATACCCCTGGTGTCTCCGG	632
Db	429	GCGAGTGTGGGATGTGACGCTGGTGAATGTTCATTTGTGTGATACCCCTGGTGTCTCCGG	488
OY	633	TATGGAATCCAGAGGAATACAAATAGAGGCACTGTTTAAATTTCACAAAAGCTTGT	692
Db	489	TATGGAATCCAGAGGAATACAAATAGAGGCACTGTTTAAATTTCACAAAAGCTTGT	548
OY	693	TACACATATGTGAAGATCATCAACTATATGATAGTCAATTTTGTCAATAGCCTGTGG	752
Db	549	TACACATATGTGAAGATCATCAACTATATGATAGTCAATTTTGTCAATAGCCTGTGG	608
OY	753	ATTCTGTGTGCTTCCAGGTCTTTCATCATTAATGATGTGTGACAGAAAGCTACGCCACTT	812
Db	609	ATTCTGTGTGCTTCCAGGTCTTTCATCATTAATGATGTGTGACAGAAAGCTACGCCACTT	668
OY	813	TTACTATCCACACAGAGTCTGGGCTCAGCTGAAAACTTAATTTTATAGGGTCAATC	872
Db	669	TTACTATCCACACAGAGTCTGGGCTCAGCTGAAAACTTAATTTTATAGGGTCAATC	728
OY	873	CTGTGTTGTTCCTTCCCTACACAGTCTTTAGATCTTAATCTTGAATGTTGTGACGAT	932
Db	729	CTGTGTTGTTCCTTCCCTACACAGTCTTTAGATCTTAATCTTGAATGTTGTGACGAT	788
OY	933	TCCAAATGCTGTAGCAGCAAGGTTTCATTTTATTAACGAATCTTCTGAGTGTAAACAGA	992
Db	789	TCCAAATGCTGTAGCAGCAAGGTTTCATTTTATTAACGAATCTTCTGAGTGTAAACAGA	848
OY	993	ATTAGCTGTATGATTTGTCTCTTCTTGTCTTTGGGGAGGCCAATGGTTTAAAGCAAAAG	1052
Db	849	ATTAGCTGTATGATTTGTCTCTTCTTGTCTTTGGGGAGGCCAATGGTTTAAAGCAAAAG	908
OY	1053	ATAATTTGGCTATAGGAATTTGTGTTTGTGCGGTTAGCCACAAACTACAGTATTCATATT	1112
Db	909	ATAATTTGGCTATAGGAATTTGTGTTTGTGCGGTTAGCCACAAACTACAGTATTCATATT	968
OY	1113	GCTTCCTTTATATTTGGGAAT-AAAAATGGGTATAGGGAGGTAAAGATGTAATTTCAATTAC	1172
Db	969	GCTTCCTTTATATTTGGGAAT-AAAAATGGGTATAGGGAGGTAAAGATGTAATTTCAATTAC	1028
OY	1172	TTGATCAAAAACAATGCTTTGATGTACCCAAAACAAAGAGCTATATAAATGCAGAAGCCTT	1232
Db	1029	TTGATCAAAAACAATGCTTTGATGTACCCAAAACAAAGAGCTATATAAATGCAGAAGCCTT	1088
OY	1232	CATTGTAGCTTATAGGATCCCTGCCCATCTGTGATATGGCGGTACAAAAGACCAAGTGT	1292
Db	1089	CATTGTAGCTTATAGGATCCCTGCCCATCTGTGATATGGCGGTACAAAAGACCAAGTGT	1148
OY	1292	TGTGGAATCCACCTGGAGTGTGCAATTAATTAATTTTCCAGTACAGATGTCTGTGTGG	1352

Db	1149	TGTTGAATCCACCTGGAGTTGCATATTATTTTTCAGTACAGAAATGCTGTGTGG	1208
Qy	1352	CCCATGAAAGAAACATAGTATTTTAAGATTTTNNAGATTTTCATTAGCTATTCAAGTTC	1411
Db	1209	CCCATGAAAGAAACATAGTATTTTAAGATTTT -AGATTTTCATTAGCTATTCAAGTTC	1267
Qy	1412	CTGTGTTGAAGCATGGTCTCTTAGGTTTGGACTGGAACCTTTAGTTCTTTTCA	1471
Db	1268	CTGTGTTGAAGCATGGTCTCTTAGGTTTGGACTGGAACCTTTAGTTCTTTTCA	1327
Qy	1532	TGCTTGGCTAACGAGTTAGATGTCCCATTCATCTCATGGCCGTAAATAAATGATAGG	1591
Db	1388	TGCTTGGCTAACGAGTTAGATGTCCCATTCATCTCATGGCCGTAAATAAATGATAGG	1447
Qy	1592	GGAGAGATATGTTAAAAATTTTCTAGGGTATCTAATCTGTAGGAAGTCACTGTCT	1651
Db	1448	GGAGAGATATGTTAAAAATTTTCTAGGGTATCTAATCTGTAGGAAGTCACTGTCT	1507
Qy	1652	AGA 1654	
Db	1508	AGA 1510	
RESULT 4			
ID	ADC86554	ADC86554 standard; DNA; 113306 BP.	
AC	ADC86554;		
DT	01-JAN-2004	(first entry)	
DE	Human GPCR gene SEQ ID NO:1007.		
XX	ds; gene; human; GPCR;		
XX	guanosine triphosphate-binding protein coupled receptor; gene therapy.		
XX	Homo sapiens.		
XX	EP1270724-A2.		
XX	02-JAN-2003.		
XX	18-JUN-2002; 2002EP-00013517.		
XX	18-JUN-2001; 2001JP-00246789.		
XX	(NMAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.		
XX	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.		
XX	Suwa M, Asai K, Akiyama Y, Aburatani H;		
XX	WPI; 2003-315783/31.		
XX	P-PSTDB; ADC86555.		
XX	New polynucleotide, useful for preparing a composition for treating a		
XX	patient in need of increased or suppressed activity or expression of the		
XX	guanosine triphosphate-binding protein coupled receptor.		
XX	Claim 1; SEQ ID NO 1007; 28bp; English.		
XX	The invention relates to a novel polynucleotide encoding a guanosine		
XX	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of		
XX	the invention may have a use in gene therapy. The polynucleotide and		
XX	polypeptide are useful for preparing a composition for treating a patient		
XX	in need of increased or suppressed activity or expression of the		
XX	guanosine triphosphate-binding protein coupled receptor. The		
XX	polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the		
XX	invention.		

XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;  
SQ  
Query Match 87.4%; Score 1472.2; DB 10; Length 113306;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
QY 155 ATGAGCTTCCCAAGTATGCTGGGCACAATACCTCCAGGAATTCCTCTTGCAATCCTAT 214  
DB 11524 AGGTGATCTTCCCAAGTATGCTGGGCACAATACCTCCAGGAATTCCTCTTGCAATCCTAT 11583  
QY 215 AGTGAACCCCACTTAATCAAGCTCTTAATAGTGTCTTAATGACGGGCTGTGGGTGT 274  
DB 11584 AGTGAACCCCACTTAATCAAGCTCTTAATAGTGTCTTAATGACGGGCTGTGGGTGT 11643  
QY 275 CATTTCAATCTTTCTCTCGGTGAAATGAACACCCGGTCAAGTACCAATGGGGGT 334  
DB 11644 CATTTCAATCTTTCTCTCGGTGAAATGAACACCCGGTCAAGTACCAATGGGGGT 11703  
QY 335 CATTAACCTGGTGGTGGTCCACAGCGTTTTCTGCTGACAGTGCATTTGGCTTGACCTA 394  
DB 11704 CATTAACCTGGTGGTGGTCCACAGCGTTTTCTGCTGACAGTGCATTTGGCTTGACCTA 11763  
QY 395 CCTCATCAAGAAAGCTTGAATGTTGGGCTGCCCTTGTGCAAAATTTGTGAGTGCATGCT 454  
DB 11764 CCTCATCAAGAAAGCTTGAATGTTGGGCTGCCCTTGTGCAAAATTTGTGAGTGCATGCT 11823  
QY 455 GCACATCCACATGTAAGCTCAAGCTCTTAATGATGATGATGATGATGATGATGATGAT 514  
DB 11824 GCACATCCACATGTAAGCTCAAGCTCTTAATGATGATGATGATGATGATGATGATGAT 11883  
QY 515 CATCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGGCTGC 574  
DB 11884 CATCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGGCTGC 11943  
QY 575 CAGTCTGGCATGTGAGCGCTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 634  
DB 11944 CAGTCTGGCATGTGAGCGCTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 12003  
QY 635 TGGATATCCATGAGGAATTCATATGAGAGCACTGTTTTAAATTTTCAAAAGAGCTTGTCTTA 694  
DB 12004 TGGATATCCATGAGGAATTCATATGAGAGCACTGTTTTAAATTTTCAAAAGAGCTTGTCTTA 12063  
QY 695 CACATATGTGAATATCAATCAATATGATGATGATGATGATGATGATGATGATGATGAT 754  
DB 12064 CACATATGTGAATATCAATCAATATGATGATGATGATGATGATGATGATGATGATGAT 12123  
QY 755 TCTGTGTGCTTCCAGGCTTTCATCATATGATGATGATGATGATGATGATGATGATGAT 814  
DB 12124 TCTGTGTGCTTCCAGGCTTTCATCATATGATGATGATGATGATGATGATGATGATGATGAT 12183  
QY 815 ACTATCCCAAGAGATTTCTGGGCTCAAGTGAAGAAACCTATTTTTTATAGGGGTGATCCT 874  
DB 12184 ACTATCCCAAGAGATTTCTGGGCTCAAGTGAAGAAACCTATTTTTTATAGGGGTGATCCT 12243  
QY 875 TGTGTGTTTTCTCCCTACAGAGTCTTATAGGATCTATTAATCTGAAATGTTGAGAGCATTC 934  
DB 12244 TGTGTGTTTTCTCCCTACAGAGTCTTATAGGATCTATTAATCTGAAATGTTGAGAGCATTC 12303  
QY 935 CAATGCTGTAGAGAGAGGTTGCAATTTATTAAGAAATCTTCTTGAATGTAACAGCAAT 994  
DB 12304 CAATGCTGTAGAGAGGTTGCAATTTATTAAGAAATCTTCTTGAATGTAACAGCAAT 12363  
QY 995 TAGCTGTATGATTTGCTTCTCTTGTCTTTGGGGGAAGCAATGGTTTAAAGCAAAAGAT 1054  
DB 12364 TAGCTGTATGATTTGCTTCTCTTGTCTTTGGGGGAAGCAATGGTTTAAAGCAAAAGAT 12423  
QY 1055 AATTGGCTTATGAAATGTTGTTGTGCGGTAGCCCAAACTACAGATTCATATTGTC 1114  
DB 12424 AATTGGCTTATGAAATGTTGTTGTGCGGTAGCCCAAACTACAGATTCATATTGTC 12483  
QY 1115 TTCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGATGATTTTCAATTACTT 1173

DB 12484 TTCTTTATATTTGGGAATTAATAATGAGGTATAGGGAGGTAAAGATGATTTTCAATTACTT 12543  
QY 1174 GATCAAAACCATATCCCTGATGTAACCAAAACAAAGACATTAATAATGCAAGGCCCTCA 1233  
DB 12544 GATCAAAACCATATCCCTGATGTAACCAAAACAAAGACATTAATAATGCAAGGCCCTCA 12603  
QY 1234 TTGTAGTCTTATGAGATCCCTCCATCTCTGAGTATGGCCGTACAAAGACCAAGTGTG 1293  
DB 12604 TTGTAGTCTTATGAGATCCCTCCATCTCTGAGTATGGCCGTACAAAGACCAAGTGTG 12663  
QY 1294 TTGAATCCACCTGAGTTCATATTAATTAATTTTCCAGTACGAATGTTGTGGGCC 1353  
DB 12664 TTGAATCCACCTGAGTTCATATTAATTAATTTTCCAGTACGAATGTTGTGGGCC 12723  
QY 1354 CATGAAGCAACATAGTTTTTAAGATTTTNGAGTTTCAATTAATGCTCATTTAAGTTCTT 1413  
DB 12724 CATGAAGCAACATAGTTTTTAAGATTTT-AGAGTTTCAATTAATGCTCATTTAAGTTCTT 12782  
QY 1414 CTGTTTGAAGCATGTCCTTATAGTTTTTGGACTGAACCTTAAGTTCTTTTCAATC 1473  
DB 12783 CTGTTTGAAGCATGTCCTTATAGTTTTTGGACTGAACCTTAAGTTCTTTTCAATC 12842  
QY 1474 CCACTTCCACATAGTAAATTTCTGGCCACACCCAGCTCCAAAGACCAAACTCTC 1533  
DB 12843 CCACTTCCACATAGTAAATTTCTGGCCACACCCAGCTCCAAAGACCAAACTCTC 12902  
QY 1534 CTTGCGTAACCAAGTTAGATGATCCCATTCATCTCAGCCCTGTAATAAAGTGAAGGG 1593  
DB 12903 CTTGCGTAACCAAGTTAGATGATCCCATTCATCTCAGCCCTGTAATAAAGTGAAGGG 12962  
QY 1594 AGAGAAATAGTTAAATTTTCTAGGGATATCATTAATCTGTTAGAAATCATCTGTCTAG 1653  
DB 12963 AGAGAAATAGTTAAATTTTCTAGGGATATCATTAATCTGTTAGAAATCATCTGTCTAG 13022  
QY 1654 A 1654  
DB 13023 A 13023  
RESULT 5  
AAFB8583  
ID AAFB8583 standard; cDNA; 1336 BP.  
XX  
AC AAFB8583;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Human GCREC-4 cDNA INCYTE ID 90012430CD1 SEQ ID 52.  
XX  
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
KW cytoabatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
KW protozoacide; clonostol; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection;  
KW gene therapy; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
PN W0200263004-A2.  
PD  
XX 15-AUG-2002.  
PF  
XX 06-FEB-2002; 2002WO-US003635.  
XX  
XX 07-FEB-2001; 2001US-0267322P.  
PR 23-FEB-2001; 2001US-0271215P.  
PR 08-MAR-2001; 2001US-0274511P.  
PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
PR 02-APR-2001; 2001US-0281107P.  
PR 06-APR-2001; 2001US-0282121P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.



XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG, Hafalia AUA;  
PI Kallik Da, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Reddy R, Butford N, Lu DM;  
PI Rankum J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;  
PI Granul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee EA, Harland L;  
XX WPI: 2002-627557/67.  
DR P-PSDB; AAB71325.  
XX  
PT New human G-protein coupled receptors (GPRC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GPRCs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
PS Claim 113; Page 212-213; 23pp; English.  
XX  
CC This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cyostatic, neuroprotective, antiparkinsonian,  
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GPRC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, cancer,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAF88580-AAF8627 encode the GPRC proteins represented by AAB71322-  
CC AAB71369, described in the disclosure of the invention  
XX  
SQ Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;  
Query Match 73.0%; Score 1228.6; DB 6; Length 1336;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1242; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 29 TCTTCTAGCATGATTTTTCACATTTAAATGAAGTTGTAGACTGATGAAGATGC 88  
DB 77 TTTTCAGCATGATTTTTCACATTTAAATGAAGTTGTAGACTGATGAAGATGC 136  
QY 89 TCAGCTAAGGAGTCTCTGATGAGCTTTAGATTGATACACCAATCCTGTAATTTGAT 148  
DB 137 TCAGCTAAGGAGTCTCTGATGAGCTTTAGATTGATACACCAATCCTGTAATTTGAT 196  
QY 149 GCAAAAATGTACTTCCCAAGTATGCTGCGCACATACCTCCAGAAATTCCTTGGCA 208  
DB 197 GCAAAAATGTACTTCCCAAGTATGCTGCGCACATACCTCCAGAAATTCCTTGGCA 256  
QY 209 TCTTATAGTGACACCCCACTTAATCAGCTCTACTTCAATAGCTTAATGGCGGAGCT 268  
DB 257 TCTTATAGTGACACCCCACTTAATCAGCTCTACTTCAATAGCTTAATGGCGGAGCT 316  
QY 269 GGGTGTATTTCCATTTCTTTTCTCTGATGAAGAAATGAACCCGGGTACAGACCAT 328  
DB 317 GGGTGTATTTCCATTTCTTTTCTCTGATGAAGAAATGAACCCGGGTACAGACCAT 376  
QY 329 GGGGTATTTACTTGT 388  
DB 377 GGGGTATTTACTTGT 436  
QY 389 GACCTTACTTCAAGAAAGATTGGAGTTGGGCTGCTTCTGCAAAATTTGAGAGTC 448  
DB 437 GACCTTACTTCAAGAAAGATTGGAGTTGGGCTGCTTCTGCAAAATTTGAGAGTC 496  
QY 449 CAGCTGACATTCACATGATCTCAGCTCTATTTCTATTTGATGATGATGATGATGAT 508  
DB 497 CAGCTGACATTCACATGATCTCAGCTCTATTTCTATTTGATGATGATGATGATGAT 556  
QY 509 ATACCTCATCTTCTTCAAGTGAAGAAAGAAAGTGAATTTCAAGAAATTCGATGCTGT 568  
DB 557 ATACCTCATCTTCTTCAAGTGAAGAAAGAAAGTGAATTTCAAGAAATTCGATGCTGT 616

QY 569 GGTGCGAGTGTCTGGCATGTGAGAGCTGTGATTTGTCAATTTGTGTACCCCTGTGTCTC 628  
DB 617 GGTGCGAGTGTCTGGCATGTGAGAGCTGTGATTTGTCAATTTGTGTACCCCTGTGTCTC 676  
QY 629 CCGGTATGAAATTCATGAGAAATATCAATGAGAGACCTGTTTAAATTTCAAAAGACT 688  
DB 677 CCGGTATGAAATTCATGAGAAATATCAATGAGAGACCTGTTTAAATTTCAAAAGACT 736  
QY 689 TGTCTTACATATGTGAAATATCAATGAGAGACCTGTTTAAATTTCAAAAGACT 748  
DB 737 TGTCTTACATATGTGAAATATCAATGAGAGACCTGTTTAAATTTCAAAAGACT 796  
QY 749 TGTGATTTCTGTGATTTCTTCCAGATCTTCAATATGATGATGATGATGATGATGAT 808  
DB 797 TGTGATTTCTGTGATTTCTTCCAGATCTTCAATATGATGATGATGATGATGATGAT 856  
QY 809 CTCTTATCATCCACAGAGATTTCTGAGCTACCTGAAATCTATTTTATATAGGAGT 868  
DB 857 CTCTTATCATCCACAGAGATTTCTGAGCTACCTGAAATCTATTTTATATAGGAGT 916  
QY 869 CATCTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 928  
DB 917 CATCTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 976  
QY 929 GCATTTCAATGCTGTGAGAGAGATTTGATTTTATATGAAATCTTCTGAGTATAC 988  
DB 977 GCATTTCAATGCTGTGAGAGAGATTTGATTTTATATGAAATCTTCTGAGTATAC 1036  
QY 989 AGCAATATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1048  
DB 1037 AGCAATATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1096  
QY 1049 AAGATATATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1108  
DB 1097 AAGATATATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1156  
QY 1109 ATTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1167  
DB 1157 ATTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1216  
QY 1168 TTAATGATCAAAACATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1227  
DB 1217 TTAATGATCAAAACATGCTGTGATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1276  
QY 1228 CCTCATTTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1274  
DB 1277 CCTCATTTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1323  
  
RESULT 6  
AAF88584  
ID ID AAF88584 standard; cDNA; 1340 BP.  
XX  
XX AAF88584;  
AC  
XX 19-NOV-2002 (first entry)  
DT  
XX  
XX Human GPRC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.  
DE  
XX  
XX GPRC, Human, G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
KW cyostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection;  
KW gene therapy; gene; ss.  
OS Homo sapiens.  
XX  
XX W0200263004-A2.  
XX  
XX 15-AUG-2002.  
XX

PF 06-FEB-2002; 2002WO-US003635.  
XX  
PR 07-FEB-2001; 2001US-0267322P.  
PR 23-FEB-2001; 2001US-0271215P.  
PR 08-MAR-2001; 2001US-0274551P.  
PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
PR 02-APR-2001; 2001US-0281107P.  
PR 06-APR-2001; 2001US-0282121P.  
XX  
PA (INCYTE GENOMICS INC.  
XX  
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
PI Kalliock DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AJA;  
PI Rankumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee BA, Harland L;  
XX  
DR MPI; 2002-627557/67.  
DR P-PSDB; AAB71326.  
XX  
PT New human G-protein coupled receptors (GPRC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GPRCs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
PS Claim 114; Page 213; 239pp; English.  
XX  
CC This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,  
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GPRC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAB8880-AAB8627 encode the GPRC proteins represented by AAB71322-  
CC AAB71369, described in the disclosure of the invention  
XX  
SQ Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;  
Query Match 65.7%; Score 1106.2; DB 6; Length 1340;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 153 AAGTGAACCTCCCAAGTATGCGCGCAATACTCCAGGAATTCCTCTGGATCCT 212  
DB 205 ACAGGTACTTCCCAAGTATGCGCGCAATACTCCAGGAATTCCTCTGGATCCT 264  
QY 213 ATAGTGACACCCCACTTAATCAGCCTCACTTCACTAGTCTTATGGCGGCTGTGGGT 272  
DB 265 ATAGTGACACCCCACTTAATCAGCCTCACTTCACTAGTCTTATGGCGGCTGTGGGT 324  
QY 273 GTCAATTCATCTTTTCTCTCTGTAATAAATGAACCCGGTCAAGTACCATGATGCG 332  
DB 325 GTCAATTCATCTTTTCTCTCTGTAATAAATGAACCCGGTCAAGTACCATGATGCG 384  
QY 333 GTCAATTCATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 392  
DB 385 GTCAATTCATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 444  
QY 393 TACCTCATCAAGAAGACTGTGATGTTGGCGCTCTGCAATATTTGTAGTGCATG 452  
DB 445 TACCTCATCAAGAAGACTGTGATGTTGGCGCTCTGCAATATTTGTAGTGCATG 504  
QY 453 CTGACATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 512  
DB 505 CTGACATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 564

QY 513 CTGATCTCTCTTCAAGTGCAAGACAAAGTGAATTCCTACAGAAATGATGCTGTGCT 572  
DB 565 CTGATCTCTCTTCAAGTGCAAGACAAAGTGAATTCCTACAGAAATGATGCTGTGCT 624  
QY 573 GCCAGTGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632  
DB 625 GCCAGTGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
QY 633 TATGGAATTCATGAGGAATTCATGAGGACATGTTTAAATTTCAAAAAGCTTGGT 692  
DB 685 TATGGAATTCATGAGGAATTCATGAGGACATGTTTAAATTTCAAAAAGCTTGGT 744  
QY 693 TACACATGATGAAATTCATCACTATGATGATGATGATGATGATGATGATGATGATG 752  
DB 745 TACACATGATGAAATTCATCACTATGATGATGATGATGATGATGATGATGATGATG 804  
QY 753 ATTCTGTGTGTCCTTCCAGGTCCTTCACTATGATGATGATGATGATGATGATGATG 812  
DB 805 ATTCTGTGTGTCCTTCCAGGTCCTTCACTATGATGATGATGATGATGATGATGATG 864  
QY 813 TTACTATCCCAAGAGAGTCTGGGCTCAGCTGAAACCTATTTTATAGGGTCAATC 872  
DB 865 TTACTATCCCAAGAGAGTCTGGGCTCAGCTGAAACCTATTTTATAGGGTCAATC 924  
QY 873 CTGTTGTGTTCCCTCCCTACAGTCTTATGAGATCATCTTGAATGTTGAGCAT 932  
DB 925 CTGTTGTGTTCCCTCCCTACAGTCTTATGAGATCATCTTGAATGTTGAGCAT 984  
QY 933 TCCATATGCTGTGACAGCAAGTGTGATTTATTAAGAAATCTTCTGAGTGTACAGCA 992  
DB 985 TCCATATGCTGTGACAGCAAGTGTGATTTATTAAGAAATCTTCTGAGTGTACAGCA 1044  
QY 993 ATTAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052  
DB 1045 ATTAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1104  
QY 1053 ATTAGTGTGTTATGGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1112  
DB 1105 ATTAGTGTGTTATGGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1164  
QY 1113 GCTTCCTTATATGGAAT-AAATGCGTATAGGGAGGTAAAGATGATTTCAATAC 1171  
DB 1165 GCTTCCTTATATGGAATAAATGCGTATAGGGAGGTAAAGATGATTTCAATAC 1224  
QY 1172 TTGATCAAAAACATGCTTATGATGATGATGATGATGATGATGATGATGATGATG 1231  
DB 1225 TTGATCAAAAACATGCTTATGATGATGATGATGATGATGATGATGATGATGATG 1284  
QY 1232 CATTTAGTCTTATGGAATCCCTCCCATCTCTGAGTATGAGC 1274  
DB 1285 CATTTAGTCTTATGGAATCCCTCCCATCTCTGAGTATGAGC 1327  
RESULT 7  
AAF88585  
ID AAF88585 standard; cDNA; 1460 BP.  
XX  
XX AAF88585;  
XX AC  
XX 19-NOV-2002 (first entry)  
XX  
DB Human GPRC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.  
XX  
XX GPRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
XX Parkinson's disease; Crohn's disease; constipation; infection;  
XX gene therapy; gene; ss.  
XX Homo sapiens.  
XX OS  
XX PN W0200263004-A2.

XX 15-AUG-2002.  
PD  
XX  
PF 06-FEB-2002; 2002WO-US003635.  
XX  
PR 07-FEB-2001; 2001US-0267322P.  
PR 23-FEB-2001; 2001US-0271215P.  
PR 08-MAR-2001; 2001US-0274551P.  
PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
PR 02-APR-2001; 2001US-0281107P.  
PR 06-APR-2001; 2001US-0282121P.  
XX  
PA (INCYTE GENOMICS INC.  
XX  
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yeo MG;  
PI Kallik DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AUA;  
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee EA, Harland L;  
XX  
DR WPI; 2002-627557/67.  
DR P-PSDB; AAB71327.  
XX  
PT New human G-protein coupled receptors (GPRC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GPRCs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
XX  
PS Claim 115; Page 213-214; 239pp; English.  
XX  
CC This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
CC hepatocarcinoma, cytotoxic, cerebroprotective, antiinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GPRC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAB8850-AAF86627 encode the GPRC proteins represented by AAB71322-  
CC AAB71369, described in the disclosure of the invention  
XX  
SQ Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;  
Query Match 65.7%; Score 1106.2; DB 6; Length 1460;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 153 AAATGTGACTTCCCAAGATGATGCTGACCAATATCTCAGGAATTCCTTGAGATCT 212  
DB 335 ACAGGTGACTTCCCAAGATGATGCTGACCAATATCTCAGGAATTCCTTGAGATCT 384  
QY 213 ATAGTACACCCCACTTAATGAGCTTACTTATGCTTATTTGGCGGCTGTGGGT 272  
DB 385 ATAGTACACCCCACTTAATGAGCTTACTTATGCTTATTTGGCGGCTGTGGGT 444  
QY 273 GTGATTTGATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTGACCACTTGGCG 332  
DB 445 GTGATTTGATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTGACCACTTGGCG 504  
QY 333 GTGATTTGATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTTGGCGTGGAC 392  
DB 505 GTGATTTGATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTTGGCGTGGAC 564  
QY 393 TACCTCATCAAGAGACTTGAATGTTGGGCTGCCCTTCTGCAATTTTGTAGTCCATG 452  
DB 565 TACCTCATCAAGAGACTTGAATGTTGGGCTGCCCTTCTGCAATTTTGTAGTCCATG 624  
QY 453 CTGCAATCCACATGATCTACTCACTTCTTATTTATGAGTATCTTGGTCAACCAATAC 512

DB 625 CTGCAATCCACATGATCTACTCACTTCTTATTTATGAGTATCTTGGTCAACCAATAC 684  
QY 513 CTGATCTTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAAATCATGCTGTGCT 572  
DB 685 CTGATCTTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAAATCATGCTGTGCT 744  
QY 573 GCCAGTCTGCAATGTGAGACCGTGTGATTTGTCAATTTGTGTAACCCCTGTTGTCTCCGG 632  
DB 745 GCCAGTCTGCAATGTGAGACCGTGTGATTTGTCAATTTGTGTAACCCCTGTTGTCTCCGG 804  
QY 633 TATGGAATCCATGAGAAATACATGAGAGACAGCTTTTAAATTTACAAAGAGCTTGT 692  
DB 805 TATGGAATCCATGAGAAATACATGAGAGACAGCTTTTAAATTTACAAAGAGCTTGT 864  
QY 693 TACACATATGTAAGAAATATCATCAATATATGATATGATATTTTGTATATGCGGTGTG 752  
DB 865 TACACATATGTAAGAAATATCATCAATATATGATATGATATTTTGTATATGCGGTGTG 924  
QY 753 ATTCTGTTGCTTCTCCAGGCTTCAATCATTTATTTGATGATGTCAGAAAGCTACGCACT 812  
DB 925 ATTCTGTTGCTTCTCCAGGCTTCAATCATTTATTTGATGATGTCAGAAAGCTACGCACT 984  
QY 813 TTACTATCCCAACAGAGATGCTGGGCTGAGCTGAAAACCTATTTTATAGGGGTATC 872  
DB 985 TTACTATCCCAACAGAGATGCTGGGCTGAGCTGAAAACCTATTTTATAGGGGTATC 1044  
QY 873 CTGTTGTTGCTTCTCCAGGCTTCAATCATTTATTTGATGATGTCAGAAAGCTACGCACT 932  
DB 1045 CTGTTGTTGCTTCTCCAGGCTTCAATCATTTATTTGATGATGTCAGAAAGCTACGCACT 1104  
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DB 1105 TCCAATGCTGTAGACAGAGATGCTGATTTATTAACGAATCTTGTAGTGTACAGCA 1164  
QY 993 ATTGAGCTGTAGATTTGCTTCTGTTGCTTGTGGGGAGACCAATGTTTAAAGCAAG 1052  
DB 1165 ATTGAGCTGTAGATTTGCTTCTGTTGCTTGTGGGGAGACCAATGTTTAAAGCAAG 1224  
QY 1053 ATAAATGCTGTAGATTTGCTTGTGCTGCTTGTAGCCATGACCAATCATATATTT 1112  
DB 1225 ATAAATGCTGTAGATTTGCTTGTGCTGCTTGTAGCCATGACCAATCATATATTT 1284  
QY 1113 GCTTCTTATATTTGGGAT-AAAATGGATATGAGGAGGTAAAGATGATTTTCAATAC 1171  
DB 1285 GCTTCTTATATTTGGGAT-AAAATGGATATGAGGAGGTAAAGATGATTTTCAATAC 1344  
QY 1172 TTGATCCAAAACAGAGCTGTGATGTACCAAAAACAAAGAGACTATTAATGAGAGCCCT 1231  
DB 1345 TTGATCCAAAACAGAGCTGTGATGTACCAAAAACAAAGAGACTATTAATGAGAGCCCT 1404  
QY 1232 CATTTGATGCTTATGAGATCCCTCCATCTCTGATGATGAGC 1274  
DB 1405 CATTTGATGCTTATGAGATCCCTCCATCTCTGATGATGAGC 1447  
RESULT 8  
AAD37670  
ID AAD37670 standard; cDNA; 1499 BP.  
XX  
XX AAD37670;  
DE 27-AUG-2002 (first entry)  
XX  
XX Human G-protein coupled receptor-6 (GPRC-6) cDNA.  
KW Human; G-protein coupled receptor-6; GPRC-6; atherosclerosis; cancer;  
KW cell proliferative disorder; gastrointestinal; autoimmune; metabolic;  
KW neurological; inflammatory; cardiovascular; viral infection; anorexia;  
KW cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;  
KW Alzheimer's disease; heart failure; hepatitis; cholelithiasis; obesity;  
KW rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;  
KW osteoporosis; gene; 88.

XX	OS	Homio sapiens.	Location/Qualifiers
XX	FH	Key	381..1400
XX	FT	CDS	/*tag= a
XX	FT		/product= "Human GCRC-6 protein"
XX	XX	MO200226825-A2.	
XX	XX	04-APR-2002.	
XX	XX	28-SEP-2001; 2001WO-US030661.	
XX	XX	29-SEP-2000; 2000US-0236546P.	
XX	PR	13-OCT-2000; 2000US-0240589P.	
XX	PR	20-OCT-2000; 2000US-0242223P.	
XX	PR	20-OCT-2000; 2000US-0243223P.	
XX	PR	03-NOV-2000; 2000US-0245855P.	
XX	PR	03-NOV-2000; 2000US-0245900P.	
XX	PR	09-NOV-2000; 2000US-0247587P.	
XX	PR	15-NOV-2000; 2000US-0249343P.	
XX	PA	(INCY-) INCYTE GENOMICS INC.	
XX	XX	Baughn MR, Graul RC, Walia NK, Gandhi AR, Hafalia AD; Rankumar J, Tribouley CM, Thornton M, Kallik DA, Yao MG, Elliott VA, Burford N, Khan PA, Yue H, Lu Y, Arvizu C, Roopa R, Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Polichy JU; WPI; 2002-426012/45.	
XX	DR	P-PSDB; AAE23414.	
XX	XX	Novel G-protein coupled receptor polypeptides referred as GCRC peptides, useful for treating multiple sclerosis, cholecystitis heart failure, angina pectoris, rheumatoid arthritis, obesity, osteoporosis.	
XX	PT	Claim 83; Page 140; 147p; English.	
XX	PS	The invention relates to human G-protein coupled receptor (GCRC 1-16) polypeptides and polynucleotides. Sequences of the invention are useful for the diagnosis, treatment and prevention of cell proliferative (e.g. cancer, Alzheimer's disease), neurological (e.g. multiple sclerosis, Huntington's disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris, heart failure), gastrointestinal (e.g. anorexia, cholecystitis), autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis) and metabolic disorders (e.g. obesity, osteoporosis), viral infections, atherosclerosis and hepatitis. GCRC proteins are useful for identifying compounds that modulate, mimic and block olfactory and taste sensations. They are also useful for identifying GCRC modulators. GCRC DNAs are useful in gene therapy. The present sequence is human GCRC-6 cDNA	
XX	XX	Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;	
XX	XX	Query Match 61.2%; Score 1030; DB 6; Length 1499;	
XX	XX	Best Local Similarity 98.6%; Pred. No. 1.3e-292;	
XX	XX	Matches 1091; Conservative 0; Mismatches 10; Indels 5; Gaps 5;	
XX	QY	157 GTGACTTCCCAAGATAGCTGGCCCAATACCTCCAGAAATTCCTTGCCATCTCTAAG 216	
XX	DB	367 GTGACTTCCCAAGATAGCTGGCCCAATACCTCCAGAAATTCCTTGCCATCTCTAAG 426	
XX	QY	217 TGACACCCCACTTATGACGCTTACTCATAGTCTTATTGGCGGGCTGGTGGTGTCA 276	
XX	DB	427 TGACACCCCACTTATGACGCTTACTCATAGTCTTATTGGCGGGCTGGTGGTGTCA 486	
XX	QY	277 TTTCATTCTTTCTCTCTGGTGAATAAACAACCCGGTCAAGTACCAACAATGGCGGTCA 336	
XX	DB	487 TTTCATTCTTTCTCTCTGGTGAATAAACAACCCGGTCAAGTACCAACAATGGCGGTCA 546	
XX	QY	337 TTAACCTGGTGGTGCACAGCGTTTTCCTGCTACAGTGCATTTGGCTTGAACCTAC 396	
XX	DB	547 TTAACCTGGTGGTGCACAGCGTTTTCCTGCTACAGTGCATTTGGCTTGAACCTAC 606	

QY	397	TCATCAGAAGACCTTGGATGTTTGGGCTGCCCCCTTCTGCAAAATTTGGAGTGCATGCTGC	456
Db	607	TCATCAGAAGACCTTGGATGTTTGGGCTGCCCCCTTCTGCAAAATTTGGAGTGCATGCTGC	666
QY	457	ACATCCACATGTACCTCAGCGTTCCTATTTCTATGTGGTGATTCCTGGTCAACAGATACCTCA	516
Db	667	ACATCCACATGTACCTCAGCGTTCCTATTTCTATGTGGTGATTCCTGGTCAACAGATACCTCA	726
QY	517	TCCTTCTTCAAGTGCMAAGACMAAAGTGGAAATTTCTACAGAAAACTGCATGCTGTGGCTGCCA	576
Db	727	TCCTTCTTCAAGTGCMAAGACMAAAGTGGAAATTTCTACAGAAAACTGCATGCTGTGGCTGCCA	786
QY	577	GTGCTGGCAGTGTGACCGCTGGTGAATTTGTCAATTGGTGATACCCCTGGTGTCTCCCCGGTATG	636
Db	787	GTGCTGGCAGTGTGACCGCTGGTGAATTTGTCAATTGGTGATACCCCTGGTGTGTCTCCCCGGTATG	846
QY	637	GAATCCATGAGGAATACATAGAGGACAGCTGTTTTTAAATTTCACAAAGACCTTGCTTTACA	696
Db	847	GAATCCATGAGGAATACATAGAGGACAGCTGTTTTTAAATTTCACAAAGACCTTGCTTTACA	906
QY	697	CATATGTGAATAATCATCACTATATGATGTATCATTTTTTGTCAATAGCCGTGTGTGAATTC	756
Db	907	CATATGTGAATAATCATCACTATATGATGTATCATTTTTTGTCAATAGCCGTGTGTGAATTC	966
QY	757	TGTTGGTCTTCCAGAGTCTTTCATCATTTATGTGTGATGGGACGAAGATACGCACTCTTTAC	816
Db	967	TGTTGGTCTTCCAGAGTCTTTCATCATTTATGTGTGATGGGACGAAGATACGCACTCTTTAC	1026
QY	817	TATCCCAACAGAGATCTGGGCTCAGCTGTGA AAAACCTAATTTTATATAGGGGTATCTCTTG	876
Db	1027	TATCCCAACAGAGATCTGGGCTCAGCTGTGA AAAACCTAATTTTATATAGGGGTATCTCTTG	1086
QY	877	TTTGTGTTCTTCCCTACCAAGTCTCTTATGATCTATTACTTGAATGTTGTGACGCATTTCCA	936
Db	1087	TTTGTGTTCTTCCCTACCAAGTCTCTTATGATCTATTACTTGAATGTTGTGACGCATTTCCA	1146
QY	937	ATGCTGTGAGAGCAAGGTGTGCAATTTTATTAACGAAATCTCTGAGGTACAGCAATTA	996
Db	1147	ATGCTGTGAGAGCAAGGTGTGCAATTTTATTAACGAAATCTCTGAGGTACAGCAATTA	1206
QY	997	GCTGCTATGATTTGCTTCTCTTTGTCTTTGGGGGAAAGCCATTTGTTTAAAGCAAAAGTAA	1056
Db	1207	GCTGCTATGATTTGCTTCTCTTTGTCTTTGGGGGAAAGCCATTTGTTTAAAGCAAAAGTAA	1266
QY	1057	TTGGCTATGGAATTTGTTGTTTGTGCCCCGTAGCCACAACTACAGTATTCATATTTGCTT	1116
Db	1267	TTGGCTATGGAATTTGTTGTTTGTGCCCCGTAGCCACAACTACAGTATTCATATTTGCTT	1324
QY	1117	CCCTTATATTTGGGAAT-AAAATGGGTATAGGGGAGGTAAGATGATTTTCATTACCTGTA	1175
Db	1325	CCCTTATATTTGGGAATAAAATGGGTATAGGGGAGGTAAGATGATTTTCATTACCTGTA	1384
QY	1176	TCAAAACATGACCTTGATGTATCCCAAAACAAAGAGATATATTAATGACAGAGCCCTCATTT	1235
Db	1385	TC-AAAGCATGCTTGATGTATCCCAAAACAAAGAGATAT-AAAATGCAAGAGCCCTCATTT	1442
QY	1236	GTAGTCCCTATAGGATCCCTCCATTC	1261
Db	1443	GTAGTCCCTATAGGATCCCTCCATTC	1468
RESULT 9			
ABK87351			
ID	ABK87351	standard; cDNA; 1051 BP.	
XX	ABK87351;		
XX	AC		
XX	DT	24-SEP-2002	(first entry)
XX	Human	Human cDNA encoding G protein-coupled receptor IGS70.	
XX	Human; ssi; gene; G protein-coupled receptor; GPCR; IGS70; CNS;		

KW	psychiatric disorder; central nervous system disorder; schizophrenia;
KW	Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
KM	heart failure; angina pectoris; myocardial infarction; kidney disease;
KM	renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
KM	inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
KM	asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
KX	osteoporosis; allergy.
OS	Homo sapiens.
FH	Key
FT	CDS
FT	60..977
FT	/tag= a
FT	/product= "GPCR IGST70"
PN	WO200244212-A2.
PD	06-JUN-2002.
PE	23-NOV-2001; 2001MO-EP013706.
PR	30-NOV-2000; 2000EP-00204280.
PR	05-DEC-2000; 2000US-0251045P.
PA	(SOLV ) SOLVAY PHARM BV.
P1	Deleersnijder W, Blockx H, De Moor L,
DR	WPI, 2002-527703/56.
XX	P-Psdb; AAU99179.
PT	Novel G-protein coupled receptor IGST70 polypeptide useful for treating
PT	dysfunctions, disorders or disease related to lung, bone marrow, spinal
PT	cord immune system.
PS	Claim 1, Page 6; 58pp; English.
XX	The invention relates to a G protein-coupled receptor (GPCR) IGST70
CC	polypeptide including sequences that are 98-99.6% identical. Also
CC	included are the polynucleotide encoding IGST70 (including sequences 98-
CC	99.6% identical to the polynucleotide or the DNA insert contained in
CC	plasmid CGS 109818), a hybridization probe derived from the
CC	polynucleotide, a DNA or RNA expression system producing IGST70, a host
CC	comprising the expression system, IGST70 receptor membrane preparation
CC	derived from the cell, an antibody immunospecific for IGST70, IGST70 is
CC	useful for diagnosing a disease or a susceptibility to disease in a
CC	subject related to expression or activity of the IGST70 polypeptide in a
CC	nucleotide sequence encoding IGST70 in the genome of the subject in a
CC	sample derived from the subject. IGST70 is also useful identifying agonist
CC	or antagonists. The IGST70 protein, polynucleotide, antibody and identified
CC	antagonists are useful for treating psychiatric and central nervous
CC	system (CNS) disorders such as schizophrenia, Alzheimer's disease,
CC	multiple sclerosis, anxiety, cardiovascular diseases such as heart
CC	failure, angina pectoris, myocardial infarction, kidney disease such as
CC	renal failure, gastrointestinal disorders such as irritable bowel
CC	syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
CC	inflammation, cancers, asthma, infection (such as bacterial, viral,
CC	fungal, protozoal) especially human immunodeficiency virus infection
CC	(HIV), diabetes, osteoporosis and allergies. The present sequence encodes
CC	the human GPCR IGST70
XX	Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;
SQ	
Query Match	58.9%; Score 991.2; DB 6; Length 1051;
Best Local Similarity	99.6%; Pred. No. 3.1e-281;
Matches 1004; Conservative	0; Mismatches 3; Indels 1; Gaps 1
Dy	215 AGTACACCCCACTTAATCACGCTTACTTAAAGTGCTTATTGGCGGGGTGGTGTGTT 274
Gy	155 ATGTGACTTCGCCAAGTAGCTGTGCACGAATACCTCCAGGAATTCCTCTTGCGATCCCAT 214
Db	44 AGGTGACTTCGCCAAGTAGCTGTGCACGAATACCTCCAGGAATTCCTCTTGCGATCCCAT 103

XX Human G-protein coupled receptor; GAVE18; signal transduction;  
 KW inflammation; physiological immunological response; antiinflammatory;  
 KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;  
 KW chromosomal mapping; tissue typing; forensic biology;  
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;  
 KW rheumatoid arthritis; gene; ds.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..918  
 FT /tag= a  
 FT /product= "GAVE18 protein"  
 XX  
 PN WO2003042399-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US035887.  
 XX  
 PR 13-NOV-2001; 2001US-0354150P.  
 PR 22-MAR-2002; 2002GB-00006891.  
 XX  
 PA (AVET ) AVENTIS PHARM INC.  
 XX  
 PI Eisingdrelo H, Cai J, Busch SJ, Gassenhuber J;  
 XX  
 DR WPI; 2003-457496/43.  
 DR P-PSDB; AAO27265.  
 XX  
 PT New GAVE18 polypeptide and nucleic acid molecule encoding the  
 PT polypeptide, useful for preventing and treating a disease or disorder  
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or  
 PT rheumatoid arthritis.  
 XX  
 PS Claim 1; Fig 5; 88pp; English.  
 XX  
 CC This invention relates to a novel G-protein coupled receptor (GAVE18)  
 CC that is involved in signal transduction in respect to inflammation and  
 CC the physiological immunological response. Molecules which may modulate  
 CC the signalling activity or signal transduction of the receptor may be  
 CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The  
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for  
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18  
 CC proteins and antibodies may be useful in screening assays, detection  
 CC assays (for example chromosomal mapping, tissue typing or forensic  
 CC biology), or predictive medicine (for example diagnostic assays,  
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The  
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse  
 CC agonist and antagonist are also useful for preventing and treating a  
 CC disease or disorder associated with aberrant expression or activity of  
 CC GAVE18, such as inflammation and immunological-related diseases or  
 CC disorders, for example asthma, chronic obstructive pulmonary disease or  
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding  
 CC the GAVE18 protein of the invention  
 XX  
 XX Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 968; DB 9; Length 1040;  
 Best Local Similarity 99.4%; Pred. No. 2.1e-274;  
 Matches 982; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 QY 171 ATGCTGGCCCAATACCTCCAGAAATCTCTTGGCATCTTAATGACACCCCACTTA 230  
 DB 1 ATGCTGGCCCAATACCTCCAGAAATCTCTTGGCATCTTAATGACACCCCACTTA 60  
 QY 231 ATCAGCCCTTACTATGATGCTTATGGCGGGCGGGGATGATTCATTCTTTTC 290  
 DB 61 ATCAGCCCTTACTATGATGCTTATGGCGGGCGGGGATGATTCATTCTTTTC 120  
 QY 291 CTCCTGTGAAATGAAACACCCGGTCACTGACCAACCATGGGCTCATTACTTGTGTG 350

DB 121 CTCCTGTGAAATGAAACACCCGGTCACTGACCAACCATGGGCTCATTACTTGTGTG 180  
 QY 351 GTCCACAGAGGTTTTTTCGTGACAGATGCCATTTGCTTGAACCTACCTCATCAGAAAGACT 410  
 DB 181 GTCCACAGAGGTTTTTTCGTGACAGATGCCATTTGCTTGAACCTACCTCATCAGAAAGACT 240  
 QY 411 TGGATGTTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGACATTCACATGTAC 470  
 DB 241 TGGATGTTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGACATTCACATGTAC 300  
 QY 471 CTACAGTTTCTTATCTATGATGATGATCTGATGATCCAGATACCTCATCTTTCAAGTGC 530  
 DB 301 CTACAGTTTCTTATCTATGATGATGATCTGATGATCCAGATACCTCATCTTTCAAGTGC 350  
 QY 531 AAAGACAAAGTGAATTCATCAGAAAATGCTAGTGTGGCTGCCAGTGTGCTGACATGTGG 590  
 DB 361 AAAGACAAAGTGAATTCATCAGAAAATGCTAGTGTGGCTGCCAGTGTGCTGACATGTGG 420  
 QY 591 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 650  
 DB 421 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 QY 651 TACATGAGAGCACTGTTTAAATTTACAAAAGAGCTTGTACACATATGTGAAATTC 710  
 DB 481 TACATGAGAGCACTGTTTAAATTTACAAAAGAGCTTGTACACATATGTGAAATTC 540  
 QY 711 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770  
 DB 541 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 QY 771 GTCTTCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 830  
 DB 601 GTCTTCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 831 TTCTGGGCTGAGCTGAAAACCTATTTTATAGGGGCTATCTTGTGTTTCTTCC 890  
 DB 661 TTCTGGGCTGAGCTGAAAACCTATTTTATAGGGGCTATCTTGTGTTTCTTCC 720  
 QY 891 TACAGTCTTTTGAATCTATCTTGAATGTTGATGATGATGATGATGATGATGATGATGATGAT 950  
 DB 721 TACAGTCTTTTGAATCTATCTTGAATGTTGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 951 AAGGTTCATTTTATACGAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1010  
 DB 781 AAGGTTCATTTTATACGAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 QY 1011 CTCTCTTCTTCTTCTTGGGGAGACCATGTTTAAAGCAAAATATATGCTTATGTAAT 1070  
 DB 841 CTCTCTTCTTCTTCTTGGGGAGACCATGTTTAAAGCAAAATATATGCTTATGTAAT 900  
 QY 1071 TGGTTTTTGGCGGTTAGCCAAACCTACAGTAATTCATTTGCTTATATTTGGGA 1130  
 DB 901 TGGTTTTTGGCGGTTAGCCAAACCTACAGTAATTCATTTGCTTATATTTGGGA 960  
 QY 1131 AT-AAATGGGTATAGGGAGGTAGGA 1157  
 DB 961 ATAAATGGGTATAGGGAGGAAAAAAA 988  
 RESULT 11  
 AAL53414  
 ID AAL53414 standard; DNA; 939 BP.  
 XX  
 AC AAL53414;  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE 939 nt coding DNA of a human G-protein coupled receptor type protein.  
 KW Anti-HIV, cyrostatic, antidiabetic, antiasthmatic, antiinflammatory;  
 KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;  
 KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;  
 KW cardiac; dermatological; antifertility; hepatotropic; antiallergic;



KM	antipneumatic; ophthalmological; antiangular; antithyroid; anticonvulsant;
KM	antirheumatic; antichrinitic; G-protein coupled receptor; subfamily I;
KM	93870 receptor; immune; inflammatory disorder; platelet disorder;
KM	skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
KM	cellular proliferative; differentiative disorder; hormonal disorder;
KM	neurological disorder; cardiovascular disorder; viral disease; pain;
KM	liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
KM	hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
KM	viral meningitis; fungal meningoencephalitis; multiple sclerosis;
KM	Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
KM	myocardial infarction; heart failure; angina pectoris; dermatitis;
KM	transcendental; rheumatoid arthritis; psoriasis; Crohn's disease;
KM	inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
KM	conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
KM	transgenic animal; human; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	
FT	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..939
FT	/*tag= a
FT	/partial
FT	/product= "human G-protein coupled receptor type protein
FT	93870"
FT	/note= "No stop codon"
PN	
PN	WO200270657-A2.
XX	
PD	12-SEP-2002.
XX	
PX	28-FEB-2002; 2002MO-US006455.
PF	
PR	01-MAR-2001; 2001US-0272677P.
PA	(MILL-) MILLENNIUM PHARM INC.
PI	
PI	Glucksmann MA;
DR	
DR	WPI; 2002-732793/79.
XX	P-RSDB; AAO22919.
PT	
PT	New G-protein coupled receptor used in receptor assays as a target for
PT	diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT	inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT	disorders.
PS	
PS	Claim 5; Page 101-103; 105pp; English.
XX	
CC	The invention relates to an isolated polypeptide, which is a G-protein
CC	coupled receptor (GPCR) related to subfamily I of G-protein coupled
CC	receptor type proteins (GPCRs), designated the 93870 receptor. The
CC	polypeptide, nucleic acid molecules and antibodies of the invention are
CC	useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC	monitoring clinical trials or pharmacogenetics), or in methods of
CC	treatment (e.g. therapeutic and prophylactic). They are useful in
CC	treating and diagnosing conditions related to aberrant activity or
CC	expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC	inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC	disorders, or bone marrow mononuclear disorders, as well as cellular
CC	proliferative and/or differential disorders, hormonal disorders,
CC	neurological disorders, cardiovascular disorders, viral diseases, liver
CC	disorders, and pain and metabolic disorders. Conditions that can be
CC	treated include cancer, diabetes mellitus, hypothyroidism,
CC	hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC	viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC	Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC	Huntington's disease, heart failure, angina pectoris, myocardial
CC	infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC	inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC	disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC	transgenic animals are useful for studying the function and/or activity
CC	of a 93870 protein and for identifying and/or evaluating modulators of
CC	93870 activities. The polynucleotides of the invention can be used in

CC	gene therapy. This polynucleotide sequence represents the 939 nucleotide
CC	DNA of the human G-protein coupled receptor type protein of the invention
XX	
SQ	Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;
Query Match	55.8%; Score 939; DB 6; Length 939;
Best Local Similarity	100.0%; Pred. No. 7,2e-266;
Matches 939;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	147 ATGCAAAAATGTGACTTCCCAAGATACCTTGSCACATACCTCCAGAAATTCCTTTCG
DB	1 ATGCAAAAATGTGACTTCCCAAGATACCTTGSCACATACCTCCAGAAATTCCTTTCG 60
QY	207 GATCCTATAGTGAACCCCACTTAATCAGCCTTACTTCAATAGTCTTAATTGCGGCTG
DB	61 GATCCTATAGTGAACCCCACTTAATCAGCCTTACTTCAATAGTCTTAATTGCGGCTG 120
QY	267 GTGGGTGTCATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCAAGACAC
DB	121 GTGGGTGTCATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCAAGACAC 180
QY	327 ATGGCGGTCAATTAATTGTGTGTGTGTGCACAGCCTTTTCTGTGACAGTGCATTCG
DB	181 ATGGCGGTCAATTAATTGTGTGTGTGTGCACAGCCTTTTCTGTGACAGTGCATTCG 240
QY	387 TTGACCTAATCTCATCAAGAAAGATTGGATGTTTGGGCTGCCCTTCTGCAATTTGTAGT
DB	241 TTGACCTAATCTCATCAAGAAAGATTGGATGTTTGGGCTGCCCTTCTGCAATTTGTAGT 300
QY	447 GCCATGTGTCACATCCACATATACCTACGCTCCATTTATGTGTGTGATCCGTGACC
DB	301 GCCATGTGTCACATCCACATATACCTACGCTCCATTTATGTGTGTGATCCGTGACC 360
QY	507 AGATACCTCAATCTTCTTCAAGTGCAGAAAGACAAAGTGAATTCACAGAAAATGTCATCT
DB	361 AGATACCTCAATCTTCTTCAAGTGCAGAAAGACAAAGTGAATTCACAGAAAATGTCATCT 420
QY	567 GTGGCTCCGATGTGTGCATATGTGACAGCTGTGATTTGTCAATGTGTGATACCCCTGTGTC
DB	421 GTGGCTCCGATGTGTGCATATGTGACAGCTGTGATTTGTCAATGTGTGATACCCCTGTGTC 480
QY	627 TCCGGGTATGGAATCCATYAGGAATACATATGAGAGACATGTTTAAATTTCACAAGAG
DB	481 TCCGGGTATGGAATCCATYAGGAATACATATGAGAGACATGTTTAAATTTCACAAGAG 540
QY	687 CTTCCTTACACATATGTGAATAATCATCACTATATATGATCAATTTTGTCAATGCCGT
DB	541 CTTCCTTACACATATGTGAATAATCATCACTATATATGATCAATTTTGTCAATGCCGT 600
QY	747 GCTGTGATTTCTTTGTGCTTCCAGGTCTTCATCATTAATTTGATGTGTGCAGAAAGCTACGC
DB	601 GCTGTGATTTCTTTGTGCTTCCAGGTCTTCATCATTAATTTGATGTGTGCAGAAAGCTACGC 660
QY	807 CACTCTTATCATCCACAGAGAGTCTGGGCTCAGCTGAAAAACCTAATTTTATATAGG
DB	661 CACTCTTATCATCCACAGAGAGTCTGGGCTCAGCTGAAAAACCTAATTTTATATAGG 720
QY	867 GTCACTCTTGTGTTGTTCTTCCCTTACAGTCTTTTAGATCTAATTAATTGAAATGTTGTG
DB	721 GTCACTCTTGTGTTGTTCTTCCCTTACAGTCTTTTAGATCTAATTAATTGAAATGTTGTG 780
QY	927 ACGCATTCGAATGCGGTGTAGCAGAAAGGTGCATTTTATAGCAAAATCTTCTGAGGTGA
DB	781 ACGCATTCGAATGCGGTGTAGCAGAAAGGTGCATTTTATAGCAAAATCTTCTGAGGTGA 840
QY	987 ACAAGCAATTAGCTGCTATGATATTTGCTTCTTGTCTTTTGGGGGAAAGCAATTTGTTAAG
DB	841 ACAAGCAATTAGCTGCTATGATATTTGCTTCTTGTCTTTTGGGGGAAAGCAATTTGTTAAG 900
QY	1047 CAAAAGTAAATTTGGCTTATAGGAATTTGTGTTTGTGCCGT 1085
DB	901 CAAAAGTAAATTTGGCTTATAGGAATTTGTGTTTGTGCCGT 939



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RESULT 12
AAL44713
ID AAL44713 standard; DNA; 918 BP.
XX
AC AAL44713;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human testis originated G-protein coupled receptor TGR10 coding sequence.
XX
KW Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
KW cytosolic; immunomodulator; cardiac; neuroprotective; gene therapy;
KW inflammation; nervous system disease; circulatory system disease; cancer;
KW metabolic disease; immunological disease; gastrointestinal disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "TGR10"
XX
PN MO200196567-A1.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-JP005061.
XX
PR 15-JUN-2000; 2000JP-00184596.
PR 19-JUN-2000; 2000JP-00223887.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Moriya T, Ito T, Shintani Y, Miyajima N;
XX
DR WPI; 2002-098071/13.
DR P-PSDB; AAM48989.
XX
PT Human testis-originated G protein-coupled receptor protein TGR10 and
PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.
PT diseases of central nervous system, inflammations and diseases of
PT circulatory system.
XX
PS Claim 5; Page 99; 110pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC novel human testis-originated G protein-coupled receptor protein TGR10.
CC The sequences can be used in the development of drugs for the treatment
CC of diseases of the central nervous system, inflammations, diseases of the
CC circulatory system, cancer, metabolic diseases, immunological diseases,
CC and diseases of the gastrointestinal system. The present sequence is the
CC coding sequence of the invention
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
XX
Query Match 54.4%; Score 916.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 3.3e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 171 ATGCGTGGCCACAAATACCTTCAGAGAAATCCTTTGCGATCCTATAGTGACACCCCACTTA 230
DB 1 ATGCGTGGCCACAAATACCTTCAGAGAAATCCTTTGCGATCCTATAGTGACACCCCACTTA 60
QY 231 ATGAGCCTCTACTTATAGTGTCTTATTTGGCGGGCTGTGGGTGTCATTTCATTTCTTTTC 290
DB 61 ATGAGCCTCTACTTATAGTGTCTTATTTGGCGGGCTGTGGGTGTCATTTCATTTCTTTTC 120
QY 291 CTCCTGGTGAAGAAAGAACCCCGGTGATGACACCAATGGCGGTGTCATTAACTTGGTGTG 350
DB 121 CTCCTGGTGAAGAAAGAACCCCGGTGATGACACCAATGGCGGTGTCATTAACTTGGTGTG 180
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QY 351 GTCACAGCGTTTTTCGTGTCAGTCAGTCATTTCCGTTGACCTTACCTTACAGAAAGACT 410
DB 181 GTCCACAGCGTTTTTCGTGTCAGTCAGTCATTTCCGTTGACCTTACCTTACAGAAAGACT 240
QY 411 TGGATGTTGGGCTGCCCTTCTGCAAAATTTTGATGTCATGCTGCAATCCACATGTAC 470
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTTGATGTCATGCTGCAATCCACATGTAC 300
QY 471 CTCACGTTCTATTTCTATGATGATCCGTTGATCCAGACAGATACCTCATCTTCAAGTGC 530
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QY 831 TTCGGGCTCAGCTGAAAAACCTATTTTTTAAGGGGTCACTCTGTTGTTCCTTCCC 890
DB 661 TTCGGGCTCAGCTGAAAAACCTATTTTTTAAGGGGTCACTCTGTTGTTCCTTCCC 720
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QY 951 AAGGTTCATTTTATATACGAATCTTCTGAGTGTAAACAGCAATTTAGCTGTATGATTTG 1010
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RESULT 13
ABA00160
ID ABA00160 standard; cDNA; 918 BP.
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AC ABA00160;
XX
DT 15-NOV-2002 (first entry)
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DE PFI-021 cDNA.
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KW Gene; human; G-protein coupled receptor; GPCR; PFI-021;
KW peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;
KW respiratory; neurology; psychology; urogenital disease;
KW reproductive dysfunction; sexual dysfunction; cancer; tissue repair;
KW dermatology; skin pigmentation; photosensit; frailty; osteoporosis;
KW metabolic disease; cardiovascular disease; sleep disorder; hair loss;
KW gastrointestinal disease; anti-infection; sensory organ disorder; ss.
XX
OS Homo sapiens.
XX
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FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "PFI-021"
XX
XX EPI225183-A2.
XX
XX 24-JUL-2002.
XX
XX 09-JAN-2002; 2002EP-00250128.
XX
XX 23-JAN-2001; 2001GB-00001739.
XX
XX (PFI2 ) PFIZER LTD.
XX (PFI2 ) PFIZER INC.
XX
XX Harland L;
XX
XX WPI; 2002-601226/65.
XX P-PSDB; AAG79446.
XX
XX New human G-protein coupled receptor involved in signal transduction,
XX useful to treat disorders associated with its expression or activity such
XX as inflammation, allergy and cancer.
XX
XX Claim 1; Fig 1; 8bp; English.
XX
XX This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.
XX Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA
XX libraries from peripheral blood mononuclear cells. Two ESTs have been
XX identified in libraries derived from breast mRNA. PFI-021 and the
XX corresponding cDNA are used to treat a patient needing altered activation
XX or expression of a GPCR, such as inflammation, allergy and respiratory,
XX neurology, psychology, urogenital disease, reproductive and sexual
XX dysfunction/disorders, cancer, tissue repair, dermatology, skin
XX pigmentation disorders, photoregulating, frailty, osteoporosis, metabolic
XX disease, cardiovascular disease, gastro-intestinal disease, anti-
XX infection, sensory organ disorders, sleep disorders and hair loss
XX
XX Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 916.4; DB 6; Length 918;
XX Best Local Similarity 99.9%; Pred. No. 3.3e-259;
XX Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX 711 ATCAACTATATGATATGATCTTTTGTGATAGCCGCTGTGATTTGTTGGTCTTCCAG 770
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XX 901 TGTGTTTGTGCGCTTAG 918
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XX AC ABT04867;
XX AC
XX DT 11-OCT-2002 (first entry)
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XX KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
XX hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN M0200242461-A2.
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XX PD 30-MAY-2002.
XX
XX PE 26-NOV-2001; 2001WO-US044386.
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XX PR 27-NOV-2000; 2000US-0253404P.
XX PR 12-DEC-2000; 2000US-0255366P.
XX PR 20-FEB-2001; 2001US-0270286P.
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XX PR 06-APR-2001; 2001US-0282358P.
XX PR 14-MAY-2001; 2001US-0290917P.
XX PR 31-JUL-2001; 2001US-0309208P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX

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DR WPI; 2002-566565/60.  
DR P-PSDB; ABJ04069.  
XX Novel endogenous and non-endogenous versions of G protein-coupled  
PT receptor useful for identification of candidate compounds as receptor  
PT agonists or antagonists for use as therapeutic agents.  
XX  
PS Claim 7; Page 56-57; 84pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC several human G-protein coupled receptors (GPCRs). These can be used in  
CC the identification of candidate compounds as receptor agonists or inverse  
CC agonists having applicability as therapeutic agents. The present sequence  
CC is a GPCR coding sequence of the invention  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;  
Query Match 54.4%; Score 916.4; DB 6; Length 918;  
Best Local Similarity 99.9%; Pred. No. 3.3e-259;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 171 ATGCTGGCCCACTACCTCCAGAAATCTCTTGGCATCCTATAGACACCCCACTTA 230  
DB 1 ATGCTGGCCCACTACCTCCAGAAATCTCTTGGCATCCTATAGACACCCCACTTA 60  
QY 231 ATCAGCCTCTACTCATAGTGTCTTATGCGGGCTGGGTGTCATTTCCATCTTTTC 290  
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QY 291 CTCTGTGTAATAAGAACACCCGGTCAAGTACCAACATGCGGTCAATTAATTGTTG 350  
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DB 841 CTTCTCTTTTCTTTTGGGGAGCCATTGTTTAAACAAAGATTAATGGCTTATGGAAT 900  
QY 1071 TGTGTTTGGCGCTTAG 1088  
DB 901 TGTGTTTGGCGCTTAG 918  
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AC ABZ59171;  
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DT 28-APR-2003 (first entry)  
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KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotoxic;  
KW anticonvulsant; hypotensive; hepatotoxic; dermatological; human;  
KW immunosuppressive; antiinflammatory; gene; ds.  
OS Homo sapiens.  
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FT /\*tag= a  
FT /product= "TGR343"  
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XX MO2003004678-A2.  
XX  
XX 16-JAN-2003.  
XX  
XX 01-JUL-2002; 2002MO-US020860.  
XX  
XX 03-JUL-2001; 2001US-0302800P.  
XX  
XX (TULAR-) TULARIK INC.  
XX  
XX Tian H, Dai K, Chen J, Zhao J, Cutler G;  
XX WPI; 2003-210368/20.  
DR P-PSDB; ABP71378.  
XX  
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
PT nephrolithiasis.  
XX  
XX  
PS Claim 7; Page 61; 74pp; English.  
XX  
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides  
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding  
CC polynucleotides. The polypeptides can be expressed by standard DNA  
CC recombinant technology. The polypeptides are useful for screening or  
CC identifying modulators of GPCR or signal transduction. The modulators of  
CC signal transduction are useful for treating or preventing TGR-associated  
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
CC polypeptides are useful as targets for diagnosing or treating e.g.  
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperproliferemia,  
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute  
CC inflammatory dermatoses. The present sequence represents a human TGR343  
CC protein encoding DNA  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 54.4%; Score 916.4; DB 8; Length 918;  
 Best Local Similarity 99.9%; Pred. No. 3.3e-259;  
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 231 ATCAGCCTCTACTTATAGTCTTATTTGGCGGGCTGTGGGTGATTTTCCATTCTTTTC 290
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QY 591 ACGCTGTGATGTGATGTGGTACCCGTTGTCTCCGGTATGAAATCCATGAGGAA 650
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QY 651 TACAATGAGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 710
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QY 711 ATCAACTATATGATATGATTTTGTCTATAGCCGTTGCTGTGATTTGTGTGCTTCAG 770
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Db 841 CTCTCTTTTGTCTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATATTTGCTTATGAAAT 900
QY 1071 TGTGTTTGTGCGGTTAG 1088
Db 901 TGTGTTTGTGCGGTTAG 918
    
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OM nucleic - nucleic search, using sw model

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9016.710 Million cell updates/sec

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Maximum Match 100%  
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	76.4	4.5	1805	US-08-405-271A-18	Sequence 18, Appl
3	76.4	4.5	1973	US-09-016-434-1391	Sequence 1391, Ap
4	76.4	4.5	1973	US-09-022-655-1417	Sequence 1417, Ap
5	76.4	4.5	3205	US-09-976-554-171	Sequence 171, Appl
6	73.2	4.3	1134	US-09-743-871B-14	Sequence 14, Appl
7	70.2	4.2	1177	US-09-743-871B-13	Sequence 13, Appl
8	62.8	3.7	1273	US-09-910-695-9	Sequence 9, Appl
9	59.8	3.6	1330	US-08-147-592A-5	Sequence 5, Appl
10	59.8	3.6	1330	US-08-292-694A-5	Sequence 5, Appl
11	59.8	3.6	1567	US-08-889-108-16	Sequence 16, Appl
12	59.8	3.6	1567	PCT-US94-10358-16	Sequence 16, Appl
13	59.8	3.6	2600	US-08-986-209A-1	Sequence 1, Appl
14	59.8	3.6	2706	US-08-454-549-1	Sequence 1, Appl
15	59.8	3.6	2706	US-08-454-552-1	Sequence 1, Appl
16	59.8	3.6	2706	US-08-676-351-1	Sequence 1, Appl
17	59.4	3.5	1143	US-09-826-509-542	Sequence 542, App
18	59.4	3.5	1182	US-09-016-434-1417	Sequence 1417, Ap
19	58.2	3.5	1452	US-08-149-093A-3	Sequence 3, Appl
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23	58.2	3.5	1452	US-09-170-311-3	Sequence 3, Appl
24	58.2	3.5	1452	US-09-473-3	Sequence 3, Appl
25	58.2	3.5	1452	US-09-048-916B-3	Sequence 3, Appl
26	58	3.4	1002	US-09-170-496D-15	Sequence 15, Appl
27	58	3.4	1002	US-09-170-496D-171	Sequence 171, App

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33	55	3.3	1000	US-08-147-592A-11	Sequence 11, Appl
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36	54.2	3.2	1155	US-09-479-130-3	Sequence 3, Appl
37	54.2	3.2	1155	US-09-472-130A-3	Sequence 3, Appl
38	54	3.2	1257	US-09-826-509-572	Sequence 572, App
39	54	3.2	1296	US-07-816-283-9	Sequence 9, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 540, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruhema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
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US-09-826-509-540

Query Match      4.5%; Score 76.4; DB 4; Length 1113;
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Oy 264 CTGTGTGCTGTCATTTCCATTTCTTTCTCTGCTGTAAGTAAGACCCGGTCACTGACC 323
Db 199 CTGGGAGACGTCCTTTCATCTGATGTCATCTTCAAGCACCAAAAGAAAGACGCACC 258
Oy 324 ACCATGCGGCTCATTTAATTGCTGTGTGTCACAGCGCTTTTGTCTGACAGTGCATTT 383
Db 259 AATATTATCATCTTTAATCACTGGCCCTGCGGACACTGTGTCCTGTCGACGCTCCCTTC 318
Oy 384 CGCTTGACCTAATCTCATGAAGAAAGACTGGATGTTGGGCTGCCCTTTCGAAATTTGNG 443
Db 319 CAGGCGACGGAACATCTCCCTCTGCGCTTTCGCGCTTGGGAATCGCTGTCAAGACAGTC 378
Oy 444 AGTGCATGTGACATCCACATGTAACCTTCACTTCTATGTATGTGATGCTGCTGTC 503
Db 379 ATTGCATGTACATCAATCAATGATGTAACCAAGCACTTCACTCACTGCAAGTGTG 438
Oy 504 ACCAGATACCTCATCTTCTTCAAGTCAAGCAAGCAAGATGGAATTTACAGAAATGTCAT 563
Db 439 GATGCGATGTACGATCTGCGACCCCATCCGTCGCTGACGCTCGGACGCTCAGCCAA 498
Oy 564 GCTGTGCTGCCAGCTGCTGACATGTGACCGCTGCTGATTTGTCAATGTGATACCCCTGTT 623
```

Db 499 GCCCAGGCTGTCATGTCGTCATCTGGGCGCTCTGTGTGGTGTCCCGTGGC 558  
Qy 624 GTCTCCCGGATGGAATCCATGAGAAATACATGAGAGCACTGTTTAAATTGACAAA 683  
Db 559 ATCATGGGCTCGGACAGGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 618  
Qy 684 GAGCTTGTACATATGTAATAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 743  
Db 619 CCTAGGATTAAGTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 678  
Qy 744 GTTGTGATGATCTGTGTGTCTTCAGGTCCTTCATCAT 781  
Db 679 CCCGTGCTGTCATCTGTGTGTCTTCAGGTCCTTCATCAT 716

## RESULT 2

US-08-405-271A-18  
; Sequence 18, Application US/08405271A  
; Patent No. 6432652  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, CHRISTOPHER J.  
; APPLICANT: KEITH, DUANE E.  
; TITLE OF INVENTION: OPIOID RECEPTOR GENES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & ROEBSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/405,271A  
; FILING DATE: 14-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20526.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030 MRSNPOERSH  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1805 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 10..1119  
; US-08-405-271A-18

Query Match 4.5%; Score 76.4; DB 3; Length 1805;  
Best Local Similarity 46.7%; Pred. No. 1.2e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;  
Qy 264 CTGCTGGGTGATCTTCATCTCTTCTCTGTAAGAAATGAAACCCGGTCAAGTACC 323  
Db 208 CTGGGGAAGTCTGCTGATGAGTATCTCCAGGACACCAAAATGAAAGACGACACC 267  
Qy 324 ACCATGCGGGTCATTAATCTTGCTGCTGCTCAAGCGTTTCTGCTGACAGTGCATTT 383  
Db 268 AATATTTCATCTTTAACTTGAAGCCCTGCGGACACTGCTGCTGCTGCTGCTGCTG 327  
Qy 384 CGCTTGAAGTACCTGATCAAGAAAGCTTGATGTTTGGGCTGCCCTTCTGCAAAATTGTG 443

Db 328 CAGGACCGGACATCTCTCGGGGCTTCTGCGCGTTTGGGAATGCGCTGACAAAGACATC 387  
Qy 444 AGTGCATGCTGCATCTCAATGATGATGATGATGATGATGATGATGATGATGATG 503  
Db 388 ATGACATTAAGTACTACAAAGATGTTTCAACAGACCTTACCTCACTGAGTGTG 447  
Qy 504 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTACAGAAACTGCAT 563  
Db 448 GATGCTAATGATGACCATCTGACCAACCCATCCGTCCTGAGGTCCGACAGTCCAGAAA 507  
Qy 564 GCTGTGCTGCGCAGTCTGCAATGTCAGTGTGATGATGATGATGATGATGATGATG 623  
Db 508 GCCCAGGCTGTCATGATGTCGATCTGGGCGCTGCTGTTGTGCTGCTGCTGCTGCTG 567  
Qy 624 GTCTCCCGGATGGAATTCATGAGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 683  
Db 568 ATCATGGGCTCGGACAGGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 627  
Qy 684 GAGCTTGTACATATGTAATAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 743  
Db 628 CTTAGGATTAAGTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 687  
Qy 744 GTTGTGATGATCTGTGTGTCTTCAGGTCCTTCATCAT 781  
Db 688 CCCGTGCTGTCATCTGTGTGTCTTCAGGTCCTTCATCAT 725

## RESULT 3

US-09-016-434-1391  
; Sequence 1391, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Selhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1391:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1973 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK



CLONE: 9471316  
US-09-016-434-1391

Query Match 4.5%; Score 76.4; DB 4; Length 1973;  
Best Local Similarity 46.7%; Pred. No. 1.3e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 264 CTGGTGGGTGTCATTTCCATTTCTTCTCTGTTGAAATGAACACCCGGTCAGTACC 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 CTGGGGAACCTGCTTGTATGATGATGATCTTCAAGGACACCAAAATGAAGACGCCACC 435
QY 324 ACCATGGCGGTGATTAATCTTGTTGGTCCAGACGCTTTTCTGTGACAGTCCATT 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 AATATTACATCTTTAACTGCGCCCTGGCCGACACTGCTGCTGACGCTGCCCTTC 495
QY 384 CGCTTGAACCTACCTCATCAAGAAAGACTTGATGTTGGGCTGCCCTTCTGCAAAATTTGTG 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 496 CAGGGACAGGACATCTCTGGGCTTCTGGCGCTTGGGAATGGGCTGTGCAAGACAGTC 555
QY 444 AGTGCATGCTGCACATCCACATGTACTCAAGTTCCTATTCTATGTTGATCTGTGTC 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 556 ATTGCCATTGACTCTACAAATGTTGACACGACCTTCACTCACTGACATGATGTG 615
QY 504 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGAAAGTGAATCTACAGAAAATGTCAT 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 616 GATGCTATGATGACATCTGCAACCCCATCCGTGCTGACGTCGACGTCAGACAA 675
QY 564 GCTGTGGCTGCGAGTGTGCGATGTGAACGCTGTGATGTCATGTTGATGATCCCTGATT 623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 676 GCCCAGGCTGTCAATGATGCGCATCTGGGCGCTGCTGTGTTGCGGTTGCCGTTGCC 735
QY 624 GTCTCCCGGTATGAAATCCATGAGAAATACAAATGAGACCTGTTTAAATTTACAAA 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 736 ATCATGGGCTCGGACAGTCCAGATGAAAGATGAGATGCTGATGATCCCTAAC 795
QY 684 GAGCTTCTTACACATATGTAATATCAATCACTATATGATGATTTTGTATAGCC 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 796 CTTAGATTTACTGGGCGCGGCTGTTGGCATCTGCACTTCTCTTCTCTTATGCTC 855
QY 744 GTTGTGTGATCTGTTGCTTTCAGGCTTTCATCAT 781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 856 CCGTGCTGTCATCTGTCTGTCTACAGCTCATGAT 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 4  
US-09-023-655-1417

; Sequence 1417, Application US/09023655  
; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/023.655

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1417:

SEQUENCE CHARACTERISTICS:

LENGTH: 1973 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9471316

US-09-023-655-1417

Query Match 4.5%; Score 76.4; DB 4; Length 1973;  
Best Local Similarity 46.7%; Pred. No. 1.3e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

```
QY 264 CTGGTGGGTGTCATTTCCATTTCTTCTCTGTTGAAATGAACACCCGGTCAGTACC 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 CTGGGGAACCTGCTTGTATGATGATGATCTTCAAGGACACCAAAATGAAGACGCCACC 435
QY 324 ACCATGGCGGTGATTAATCTTGTTGGTCCAGACGCTTTTCTGTGACAGTCCATT 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 AATATTACATCTTTAACTGCGCCCTGGCCGACACTGCTGCTGACGCTGCCCTTC 495
QY 384 CGCTTGAACCTACCTCATCAAGAAAGACTTGATGTTGGGCTGCCCTTCTGCAAAATTTGTG 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 496 CAGGGACAGGACATCTCTGGGCTTCTGGCGCTTGGGAATGGGCTGTGCAAGACAGTC 555
QY 444 AGTGCATGCTGCACATCCACATGTACTCAAGTTCCTATTCTATGTTGATCTGTGTC 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 556 ATTGCCATTGACTCTACAAATGTTGACACGACCTTCACTCACTGACATGATGTG 615
QY 504 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGAAAGTGAATCTACAGAAAATGTCAT 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 616 GATGCTATGATGACATCTGCAACCCCATCCGTGCTGACGTCGACGTCAGACAA 675
QY 564 GCTGTGGCTGCGAGTGTGCGATGTGAACGCTGTGATGTCATGTTGATGATCCCTGATT 623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 676 GCCCAGGCTGTCAATGATGCGCATCTGGGCGCTGCTGTGTTGCGGTTGCCGTTGCC 735
QY 624 GTCTCCCGGTATGAAATCCATGAGAAATACAAATGAGACCTGTTTAAATTTACAAA 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 736 ATCATGGGCTCGGACAGTCCAGATGAAAGATGAGATGCTGATGATCCCTAAC 795
QY 684 GAGCTTCTTACACATATGTAATATCAATCACTATATGATGATTTTGTATAGCC 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 796 CTTAGATTTACTGGGCGCGGCTGTTGGCATCTGCACTTCTCTTCTCTTATGCTC 855
QY 744 GTTGTGTGATCTGTTGCTTTCAGGCTTTCATCAT 781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 856 CCGTGCTGTCATCTGTCTGTCTACAGCTCATGAT 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5  
US-09-976-594-171

; Sequence 171, Application US/09976594  
; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976.594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

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; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 171
; LENGTH: 3205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 222181.1
US-09-976-594-171
```

```
Query Match 4.5%; Score 76.4; DB 4; Length 3205;
Best Local Similarity 46.7%; Pred. No. 1.7e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
```

```
QY 264 CTGTGGGTGTCATTTTCATTTCTTCTCTGTGTAATAAGAACCCGGTCAGTACC 323
    |||||
DB 450 CTGGGGAACCTGCTTGCATGTACGTATCCTCAGGACACCAAAATGAAGACGCCACC 509
    |||||
QY 324 ACCATGCGGTGTCATTTACTTGTGTGTCACAGCGTTTCTGTGACAGTGCATTT 383
    |||||
DB 510 AATTTTACATCTTTTACCTGTGCGCCCTGCGGACACTGTGCTGTGACGCTGCCCTTC 569
    |||||
QY 384 CGCTTGAACCTACCTCATCAAGAAAGCTTGATGTTTGCGCTGCCCTTCTGCAATTGTG 443
    |||||
DB 570 CAGGGACAGGACATCTCTGCGGCTCTGGCGGTTTGGAAATGGCTGTGCAAGACAGTC 629
    |||||
QY 444 AGTGCCTGTGTCATCTACATGATGATCTTCACTTCTATTTATGTTGATCTGTGTC 503
    |||||
DB 630 ATTGCCATTGACTACTTCAACATGTTTCCACGACACCTTCACTTCACTGCAATGATGTG 689
    |||||
QY 504 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGAAATGGAATTTCTACAGAAACTGCAT 563
    |||||
DB 690 GATGCGTATGTAGCAATCTGCCACCCCATTCGTCCTCGAGCTCGCAGCTCAGCAAA 749
    |||||
QY 564 GCTGTGCTGCTCCAGTGTGTCATGTGACGCTGTGATGTTCATTTGTGATACCCCTGTT 623
    |||||
DB 750 GCCCAGGCTGTGATGTGCGCATCTGGGCCCTGCGCTGTGTGTGCGTGTTCGCTTGGCC 809
    |||||
QY 624 GTCTCCCGGTATGATTCATGAGGATATCAATGAGAGCACTGTTTAATTTACAAA 683
    |||||
DB 810 ATCATGGGCTCGGACAGTGCAGAGATGAAGATCAGATGCTGTGAGATCCCTACAC 869
    |||||
QY 684 GAGCTTCTTACACATATGTGAATAATCATCAACTATATGATGATTTTTCATATGCC 743
    |||||
DB 870 CCTCAGATTAATCTGGGCGCCGGGTGTTGCCATCTGCATCTTCTTCTTCATATGTC 929
    |||||
QY 744 GTTGTGCTGATCTGTGTGCTTCTCCAGTCTTCATCAT 781
    |||||
DB 930 CCGGTGCTGATCTGTGTGCTGTGTAAGGCTATGAT 967
    |||||
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```
RESULT 6
US-09-743-871B-14
; Sequence 14, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUS
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743,871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093,002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1134
; TYPE: DNA
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; ORGANISM: homo sapiens
US-09-743-871B-14
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Query Match 4.3%; Score 73.2; DB 4; Length 1134;
Best Local Similarity 46.8%; Pred. No. 8.5e-12;
Matches 231; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
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QY 288 TTCTCCTGTGTAATAAGAACCCGGTCAGTACCAACATGAGCGGTATTAATCTTGTC 347
    |||||
DB 223 TGCTTGTATGTACACACCAAAATGAAGACGACCAATTTTACATCTTTAACCTGGCC 282
    |||||
QY 348 GTGCTCCACAGCGTTTTTCTGTGACAGTGCATTTTGTGTTACCTTCAATCAAGAG 407
    |||||
DB 283 CTGGCGACACTCTGTGCTGTGACGCTGCCCTTCCAGGGACAGGACATCTCTGGGC 342
    |||||
QY 408 ACTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGAGCCATGTGCAATCCACATG 467
    |||||
DB 343 TTCTGGCCGTTTGGAAATGGCTGTGCAAGACGATTTGCCATTGACTTACATCAACATG 402
    |||||
QY 468 TACCTCACTTCTATTTATGATGATCTGTGACAGATTAACCTCATCTTCTCAAG 527
    |||||
DB 403 TTACCAAGACCTTCACTTCACTGCAATGATGATGATGATGATGATGATGATGATG 462
    |||||
QY 528 TGCAAGACAAAGTGAATTTTACAGAAACCTGATGCTGTGCTGCTGCTGCTGCTG 587
    |||||
DB 463 CCCATCGTGCCTTCGACGTCGCAAGTCCAGCAAGAAAGCCAGGCTGTGATGTGCGCATC 522
    |||||
QY 588 TGAACGCTGTGATTTGTGATTTGTGATACCCCTGTGTGCTCCCGGTATGGAATCCATGAG 647
    |||||
DB 523 TGGGCCCTGGCTCTGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 582
    |||||
QY 648 GAATACATATGAGGACAGCTTTTAAATTTCAAGAAAGCTTCTTACATATGTAATA 707
    |||||
DB 583 GATGAAGATGCAAGTGCCTGTGTGAGATCCCTTACAGATTAATCTTGGGCGCCGGT 642
    |||||
QY 708 ATCATCACTATATGATGATTTTGTGATGATGATGATGATGATGATGATGATGATG 767
    |||||
DB 643 TTGTCATCTGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 702
    |||||
QY 768 CAGTCTTATCAT 781
    |||||
DB 703 TACAGCCTCATGAT 716
    |||||
```

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RESULT 7
US-09-743-871B-13
; Sequence 13, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOU
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743,871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093,002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-743-871B-13
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Query Match 4.2%; Score 70.2; DB 4; Length 1177;
Best Local Similarity 46.6%; Pred. No. 7.5e-11;
Matches 225; Conservative 0; Mismatches 258; Indels 0; Gaps 0;
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QY 299 GAAATGAAACACCCGGTGAAGTACCAATGGCGGTATTAATCTGTGTGTGTCACAG 358
    |||||
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Db 277 GCACACCAAAATGAGACAGCCACCAATTTATCATCTTAACTGGCCCTGGCCGACAC 336  
Qy 359 CGTTTTCGCTGACAGTGCATTTGGCTTGAACCTCATCTCAAGAAAGACTTGGATTT 418  
Db 337 TCTGCTCTGCTGACGCTGCTCTTCAAGGACGACATCTCTGGCCGTT 396  
Qy 419 TGGGCTGCTCTTGCAGAAATTTGTAGTGCATGCTGCACATCCACATGATCCTGCTT 478  
Db 397 TGGGAATGCGCTGTCAGAGACATGCTTGCATTAACATCAACATGTTTACACGAC 456  
Qy 479 CCTATTATGATGCTGATCTCTGTCACAGATACCTCATCTTTTCAAGTGCAAGACAA 538  
Db 457 CTTCACCTTAACCTGACATGATGATGCTATGATACATCTCCACCCCATCTGTC 516  
Qy 539 AGTGAATTTCAAGAAATCTGCAATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598  
Db 517 CCTGACGCTGCGACGTCACAGAAAGCCAGGCTGTCAATGAGGCACTTGGCCCTGAC 576  
Qy 599 GATTGTCAATGCTGACCCCTGCTGTCTCCCGATGGAATCCATGAGAAATACATGA 658  
Db 577 CTCTGTCTCGGTGTCTCCCTGCTGATGAGGCTGCGACAGGTCGAGATGAGAT 636  
Qy 659 GAGCACTGTTTAAATTTCAAAAGAGCTTGTCAATATGTAATGTAATCATCACTA 718  
Db 637 CGAGTGCCTGCTGAGATCCCTACCCCTCAAGATTAAGGAGCCCGGTGTTGACATCTG 696  
Qy 719 TATGATAGTCAATTTTGTCAATAGCCGTGCTGTATTTGTTGCTTTCAGGCTTAT 778  
Db 697 CATCTTCTCTTCTCTTCAATGCTGCTCCGCTGTCTGTCTGTCTGTCTGTCTGTCT 756  
Qy 779 CAT 781  
Db 757 GAT 759

RESULT 8  
US-09-910-695-9  
Sequence 9, Application US/09910695  
Patent No. 6737252  
GENERAL INFORMATION:  
APPLICANT: Hedrick, Joseph A.  
Vicari, Alain P.  
Zlotnick, Albert  
TITLE OF INVENTION: Mammalian Chemokines; Receptors;  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/910,695  
FILING DATE: 20-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/122,585  
FILING DATE: 24-JUL-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0757  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1273 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 429..1238  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 60/053,693  
FILING DATE: 25-JUL-1997  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-910-695-9

Query Match 3.7%; Score 62.8; DB 4; Length 1273;  
Best Local Similarity 45.7%; Pred. No. 1.5e-08;  
Matches 255; Conservative 0; Mismatches 302; Indels 1; Gaps 1;

Qy 227 CTATATAGCTCTTACTTCAATGCTTATTTGGCGGGCTGGTGGTGCATTTTCATTTCT 286  
Db 321 CCTAGTCTTTCACAGCTGCAATCTTCGATGGGCTGTGTTTATGATGCTGCGTTGTG 380  
Qy 287 TTCTCCTGCTGAAATGAAACACCGGTCAGTACACCAATGGCGGTCATTATCTTGT 346  
Db 381 GGTTTAAGCTGTACGACCAAGAAAGACAG-TCACATCTACATGATGAACGTTGC 439  
Qy 347 GGTGTCACAGCGTTTTCGTCTGCTGACAGTGCATTTGCTTGAACCTCATCAAGAA 406  
Db 440 ACTACTGACCTGTATTTATACATGATGCGCTTTCGATGTTTATGATGCAAGAG 499  
Qy 407 GACTTGATGTTTGGGCTGCTTTCGAATTTGTAGTGCATGCTGCATTCAT 466  
Db 500 CGAGTGCATTTGAGAGTACTTCCACATTTCTGGGGCCCTGCTGTGTTTACCC 559  
Qy 467 GTACCTCAGCTCTTATTTATGATGATCTGTCACAGATACCTCATCTTCTTCAA 526  
Db 560 AAGCTCTGCTGTGGCTTCTTGTCTTATGATGCTGACAGATACAGGCTCATGTA 619  
Qy 527 GTGCAAGACAAAGTGAATTTTACAGAAATGCTGATGCTGCTCCAGTGTGCAT 586  
Db 620 GCCAAATATGCAAGAGCTGAAGAAACACGGAGGCGGTGCTGCTGTGGGGGT 679  
Qy 587 GTGACCTGCTGATTTGTCTATTTGTGTAACCTTGTGTCTCCGGTATGAAATCA 646  
Db 680 CTGGTATGACCTTGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739  
Qy 647 GGAATCAATGAGAGACGTTTAAATTTCAAAAGACTTGTCTTACATATGTA 706  
Db 740 TGCTCTCTCCCGCCACCTGCTGAGATCTCGATCAACCACTTAAAGCTGCA 799  
Qy 707 AATCATCACTATATGATGATGATTTTGTATAGCGGTGTGTGATTTCTGTGCTT 766  
Db 800 CGTCTCACTTACAGGATCATATTTTCTTCGATCCCTTGTTCATGATGATCG 859  
Qy 767 CCAAGTCTCATATAT 784  
Db 860 GTGCTACGTGTCATCAT 877

RESULT 9  
US-08-147-592A-5  
Sequence 5, Application US/08147592A  
Patent No. 6096513  
GENERAL INFORMATION:  
APPLICANT: Bell, Graeme I  
APPLICANT: Reisine, Terry  
APPLICANT: Yasuda, Kazuki  
TITLE OF INVENTION: Opioid Receptor Genes,  
TITLE OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,592A  
FILING DATE: 05-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30-JUL-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 161..1261  
US-08-147-592A-5

Query Match 3.6%; Score 59.8; DB 3; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 1.4e-07;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

179 CCAGAAATACCTCCAGGAATTCCTTGGGATCCTATATGTGACACCCCACTTAATACGCT 238  
262 CCTCAATGCTAGCCACAGTGCCTTCCGCCCTTGAAGTCAACATCGGGGCT 321  
239 CTACTTCATAGTGCTTATTTGGCGGGCTGTTGGG--TGTCAATTCATTTCTTTCCCTCT 295  
322 CTACTTGGCTGTGTGCAATCGGGGGCTCTCGGGAACTGCTCTGTAATGATGTCATCT 381  
296 GGTGAAATGAAACCCGGTCAATGACCAACCATGCGGTCATTAATCTGTGTGTGCA 355  
382 CAGGCAACCAAGATGAAGCTGTACCAATTAATTAATGATGGGACGTGA 441  
356 CAGGCTTTTCTGTGACAGTGCATTTGCTTGAATCTTCAAGAAAGACTTGAT 415  
442 TACCTGATCTGTGTGACACTGCCCTTCCAGGGCAGACATCTTGTGGGCTTCTGCC 501  
416 GTTTGGGCTGCCCTTGGCAAAATTTGTGAGTGCATGCTGACATCCACATGTACCTCAC 475  
502 ATTTGGGAATGACATGTGCAAGACGGTCATTTGATGACTACATCAACATGTTTACAG 561  
476 GTTCTATTTGATGTGTGATCTGTGACACAGATACCTCATCTTCTTCAAGTCAAGA 535  
562 CACTTTCATTTGACTGCAATGAGTGTGAACCGTTATGTAGCTATCTGCCACCTATCCG 621  
536 CAAAGTGAATTTACAGAAAATGCAATGCTGTGTGTGCGCAAGTCTGGCATGTGACGCT 595  
622 TGCCCTTGAATGTGACATCACTAAGTAAGCCAGGCGGTTAATGTGACCATATGGGCTCT 681

596 GGTGATTTGATGTGTGATACCCCTGGTGTCTCCCGTATGATGATCATGAGGAATACAA 655  
682 GGCTTGGTGTGTGTGTGTCTTCTTCCATCATAGGCTCAGCAACATGAGATGAAGA 741  
656 TGAGAGCACTGTTTAAATTTCAAAAGACTTGCTTACACATATGTAAATCATCA 715  
742 GATGAGTGTGTGTGAGATCCCGCCCTCAGACATATGGGGCCGTGTATTTGCCAT 801  
716 CTATATGATGATCATTTTGTGATAGCGTGTGATGATTTGTTGCTTCCAGGTCTT 775  
802 CTGATCTTCTCTTTTCTTCTTCAATCCGGTGTGATCATCTGTGTGCTACAGCT 861  
776 CATCAT 782  
862 CATGATT 868

RESULT 10  
US-08-292-694A-5  
Sequence 5, Application US/08292694A  
Patent No. 6319686  
GENERAL INFORMATION:  
APPLICANT: BELL, GRAEME  
APPLICANT: REISINE, TERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,694A  
FILING DATE: August 19, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20 May 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 July, 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 5 No. 6319686ember 1993  
FILING DATE: 08/147,592  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US94/05747  
FILING DATE: 20 May 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS

LOCATION: 161..1261  
US-08-292-694A-5

Query Match 3.6%; Score 59.8; DB 3; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 1.4e-07;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

```
QY 179 CCNAAATACCTCCAGAAATTCCTCTTGAGATCTATATGACACCCCACTTAACAGCT 238
DB 262 CCTAAATGCTACCAAGTCCCTTCCTGCCCCCTTGAGCTCAAGGTCAACATGCGAGCT 321
QY 239 CTACTTATAGTGTCTATTTGCGGGCTGATGGG---TGTCATTTTCAATTTCTTCTCT 295
DB 322 CTACTTGGCTGTGTGATCGGGGGCTCTCTGGGAACCTGCTGCTATGATGATCTCT 381
QY 296 GGTAAATATGAACCCCGTACAGTACCAACATGCGGTCTATTAATCTGTGTGTGCA 355
DB 382 CAGGACACCAAGATGAAGACTGCTACCAATTTATCTGACATGCGACTGGCTGA 441
QY 356 CAGGTTTTCTGTGACAGTCCATTTGCTTGAACCTCATCAAGAAAGACTTGAT 415
DB 442 TACCTGCTCTGTGACACTGCCCCCTTCAGGGACAGACATCTTCTGGGCTTCTGACC 501
QY 416 GTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATGTCAGATCCACATGTACTGAC 475
DB 502 ATTTGGGAATGACTGTGCAAGACGCTCATTTGATGACTATCAACATGATTTACAG 561
QY 476 GTTCTATTTCTATGTGTGATCTGTGTCACCAATACCTCATCTTCTTCAAGTCAAGA 535
DB 562 CACTTTCATTTGACTGCAATGATGATGACCGTTATGATGATCTTCTGCAACCTTACCG 621
QY 536 CAAATGGAATTTCAAGAAATGCTGCTGTGGCTGCGAGTCTGCAATGTGAGCT 595
DB 622 TGCCCTTGTGTGACATCCAGTAAAGCCAGCGGTATATGTGCGCATATGCGCCCT 681
QY 596 GGTATTTGCTATGTGATGATCCCTGTGTCTCCCGGATGAAATTCATGAGAAATCAA 655
DB 682 GGTCTGCTGTGTGTGCTTCTGTGCTATGATGAGCTCAAGCAAGTGAAGTGAAGA 741
QY 656 TGAGAGACACTGTTTAAATTTCAAAAGCTTGTCTTACATATGATGAAATCATCA 715
DB 742 GATGAGATGCTGTGAGATCCCGCCCTCAGAGACTATGGGGCCCTGATTTGCGAT 801
QY 716 CTATATGATGATCTTTTGTGATGCGCTGTGTGATTTGTGTGCTTCCAGTCTT 775
DB 802 CTGATCTTCTTCTTCTTCTTCTATCATCCCGTCTGATCATCTGTGTGCTGACGCT 861
QY 776 CATCAT 782
DB 862 CATGATT 868
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## RESULT 11

US-08-889-108-16  
; Sequence 16, Application US/08889108  
; Patent No. 6103492  
; GENERAL INFORMATION:  
; APPLICANT: Yu, lei  
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/305,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005\WIM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1567 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 173..1273

US-08-889-108-16

Query Match 3.6%; Score 59.8; DB 3; Length 1567;

Best Local Similarity 45.6%; Pred. No. 1.5e-07;

Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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QY 235 GCGCTACTCATAGTCTTATTGGGGGCTGATGGG---TGTCATTTCCATTTCTTCC 291
DB 330 GGGCTACTTGTGCTGTGTGATCGGGGGCTCTCTGGGAACCTGCTGTATGATGTCA 389
QY 292 TCCGTGAAATGAACACCCGTCAGTACCAACATGCGGTCTATTAATCTGTGTG 351
DB 390 TCCGACGGACACCAAGATGAAGACGCTACCAATTTATATTTATCTGCACTGG 449
QY 352 TCCAGACGCTTTTCTGTCTGACAGTGCATTTGCTTGAACCTTCAAGAACTT 411
DB 450 CTGATACCTCGGTCTGTCTAAGCTGCCCTTCCAGGGACAGACATCTTCTGCGCTTCT 509
QY 412 GGAATTTGGGCGCCCTTCTGCAAAATTTGTAGTGCATGTCAGATCCATGACATGATACC 471
DB 510 GGGCATTTGGGAATGCACTGTGAAGCTGTCAATGCTATGCACTATTAACAATGTTTA 569
QY 472 TCACTTCTATTTCTATGTGTGATCTGTGTCACAGATACCTCATCTTCTTCAAGTCA 531
DB 570 CCAAGCACTTTTACTGTAGACCGCATAGAGGTACACGGCTATGTGGCTATGCAACCTTA 629
QY 532 AAGACAAAGTGAATTTCAAGAAACTGATGCTGTGCTGCGAGTGTGCAATGTGA 591
DB 630 TCCGTGCCCTTGAATGTGCGACATCCAGCAAAACCCAGCGCTGTAAATGTGGCATATGGG 689
QY 592 CGCTGGATTTGATTTGTGATGATCCCTGTGTCTCCCGGTATGAAATCATGAGGAAT 651
DB 690 CCGTGGCTTGAAGTGTGTGTGCTGTGTGCTATGATGATGATGATGATGATGATGATG 749
QY 652 ACAATGAGACACTGTTTAAATTTCAAAAGCTTGTCTTACATATGATGAAATCA 711
DB 750 AAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 809
QY 712 TCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
DB 810 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869
QY 772 TCTTCAAT 782
DB 870 GCGTCATGATT 880
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## RESULT 12

PCT-US94-10358-16  
; Sequence 16, Application PC/TUS9410358



Db 820 GGCCTTCGGTGGTGGTGTTCCTGTCATATGCGCTCAGACAAAGTGGAGAGAGA 879  
QY 656 TGAGAGACACTGTTTAAATTTACAAAGAGCTTGCTTACATATGGAATAATCA 715  
Db 880 GATCAGAGCGCTGGTGGAGATCCGCCCTCAGAGACTATTGGGCCCTGTATTTGCCAT 939  
QY 716 CTATATGATAGTCAATTTTGTGATAGCGGTTGCTGTGATTCGTGTGCTTCCAGTCTT 775  
Db 940 CTGCATCTTCTTTTCTTCTTCATCATCCGGTCTGATCACTCTGTCTGTACAGCCT 999  
QY 776 CATCAT 782  
Db 1000 CATGATT 1006

RESULT 14  
US-08-454-549-1  
; Sequence 1, Application US/08454549  
; Patent No. 5866324  
; GENERAL INFORMATION:  
; APPLICANT: EPPLE, C. Mark  
; APPLICANT: OZENBERGER, Bradley A.  
; APPLICANT: HULMES, Jeffrey D.  
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
; TITLE OF INVENTION: TO OPIOID RECEPTORS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby, P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,549  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph R.  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 527-7700  
; TELEFAX: (212) 753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2706 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Rat brain  
; US-08-454-549-1

Query Match 3.6%; Score 59.8; DB 2; Length 2706;  
Best Local Similarity 45.6%; Pred. No. 2.2e-07;  
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

QY 235 GCCTCTACTTCAATGCTGTTATGGCGGCTGGTGGG---TGTCAATTCATTTCTTTC 291  
Db 264 GGCCTTACTTGGCTGTGTGCAATCGGGGGCTCTCTGGGAAGTGCCTGTGATGTATGCA 323  
QY 292 TCTGTGTAATAATGAACCCGCTCAGTGACCAACATGCGCTATTAACTTGCTGGTGG 351  
Db 324 TCTCAGGACACCAAGATGAAGACAGTACCAATTATTAATCTGCACTGG 383

QY 352 TCACAGCGTTTCTGTGTACAGTGCATTTGCGCTTGACCTACCTCATCAAGAAGCTT 411  
Db 384 CTGATACCCCTGTGTGTCTAACTGCTCCAGGGACAGACATCTTACTGGGCTTCT 443  
QY 412 GGATGTTTGGGCTGCCCTTGTGCAAAATTTGTGAGTGCATGTGCAATTCACATGTAC 471  
Db 444 GGCATTTTGGGAATGCACTGTGCAAGACTGTGATTTGCTATGTGACTTACAACTGT 503  
QY 472 TCAGTTCCTATTCTATGTGTGATCTGTGTACCAAGATACCTGATCTTCTTCAAGTCA 531  
Db 504 CCAGACTTTTACTCTGACCGCCATGAGCGTGAACCGCTATGTGGTATCTGCCACCTA 563  
QY 532 AAGACAAAGTGAATTTCAAGAAAATGCAATGCTGTGCTGCCAGTGTGGCATGTGGA 591  
Db 564 TCCGTGCCCTTGATGTGAGCATCCAGCAAGCCAGCGCTTTAAATGTGCCATATGAGG 623  
QY 592 CGCTGTGATTTGTATTTGGTACCCCTGGTGTCTCCCGGTATGATCATGAGGAAT 651  
Db 624 CCTGGCTTCAGTGTGTGTGTCTGTGTCATCATGAGGTTCAAGCAAGTGAAGATG 683  
QY 652 ACAATGAGAGCACTGTTTAAATTTCAAAAGACTTGTCTTACACATATGTGAATAATCA 711  
Db 684 AAGAGATCGAGTGTCTGTGGAATCCCTGCCCCAGAGACTATTGGGGCCCTGTATTGG 743  
QY 712 TCAACTATATGATGATGATTTTGTCAATAGCCGTGCTGTGATTTCTGTGCTTCAAG 771  
Db 744 CCATCTCATCTTCTTCTTTTCTTCTTCAATCATCCCTGTGCTGATCATCTGTCTGTACA 803  
QY 772 TCTTCATCAT 782  
Db 804 GCCTCATGATT 814

RESULT 15  
US-08-454-552-1  
; Sequence 1, Application US/08454552  
; Patent No. 6005072  
; GENERAL INFORMATION:  
; APPLICANT: EPPLE, C. Mark  
; APPLICANT: OZENBERGER, Bradley A.  
; APPLICANT: HULMES, Jeffrey D.  
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
; TITLE OF INVENTION: TO OPIOID RECEPTORS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby, P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,552  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph R.  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 0646/1A818-US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 527-7700  
; TELEFAX: (212) 753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2706 base pairs  
; TYPE: nucleic acid





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 01:56:38 / Search time 6088.21 Seconds  
(without alignments)  
10528.586 Million cell updates/sec

Title: US-10-085-233B-1

Perfect score: 1684

Sequence: 1 tcgcagcagtcacacattt.....cttatgcagtcagtcgagcg 1684

Scoring table: IDENTITY NUC

Search: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_est3.\*

4: gb\_est4.\*

5: gb\_est5.\*

6: gb\_est6.\*

7: gb\_est7.\*

8: gb\_est8.\*

9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678.8	40.3	694	7	CO918710 AGNCOURT
2	644.4	38.3	684	9	AG145972 Pan trogl
3	642.2	38.1	717	7	CO918845 AGNCOURT
4	415.8	24.7	772	2	BF160725 BPI60725
5	354.2	21.0	580	8	AZ554824 RPI-23-2
6	338	20.1	456	8	AQ888495 HS_3162_B
7	325.8	19.3	678	5	BX952455 DKFZp781N
8	280.6	16.7	306	7	CV329473 CV329473
9	237.2	14.1	646	4	BG862323 BG862323
10	203	12.1	499	6	CD699779 EST16303
11	199	11.8	478	4	BG145683 mac3c07
12	181	10.7	649	4	BG461295 RST44080
13	162	9.6	283	4	BG221739 RST41554
14	146.2	8.7	2774	3	AK041317 Mus muscu
15	142	8.4	834	1	AJ455645 AJ455645
16	142	8.4	834	1	AJ455645 AJ455645
17	104	6.2	680	6	CA355790 627748 NC
18	104	6.2	680	6	CA355790 627748 NC
19	103.6	6.2	644	7	CF906232 A0448D05-
20	90.6	5.4	598	7	CF906232 A0448D05-
21	86.4	5.1	529	5	BU698671 A0438B06-
22	82	4.9	661	6	BY748361 L21n1411
23	76.2	4.5	705	6	BY748361 BY748361
24	72.2	4.3	733	6	CA050323 Leuko82.2

25	71.4	4.2	648	6	CB514250	CB514250
26	70	4.2	659	9	B0563030	B0563030
27	70	4.2	996	9	AY401267	AY401267
28	69.8	4.1	879	9	AY410745	AY410745
29	69.4	4.1	866	6	CD246184	CD246184
30	69.4	4.1	980	4	BM543468	BM543468
31	68.6	4.1	542	6	CA965628	CA965628
32	67	4.0	672	7	CO957761	CO957761
33	64.4	3.8	671	5	BY752012	BY752012
34	62.6	3.7	353	5	BY183952	BY183952
35	61.2	3.6	679	6	BY750559	BY750559
36	60.2	3.6	785	4	BI754749	BI754749
37	60	3.6	450	6	CA576592	CA576592
38	60	3.6	607	2	BB634972	BB634972
39	60	3.6	689	6	BY751880	BY751880
40	59.8	3.6	2919	3	AK038620	AK038620
41	59.8	3.6	2959	3	AK079529	AK079529
42	59	3.5	695	6	BY751732	BY751732
43	58	3.4	718	7	CO570572	CO570572
44	58	3.4	791	6	CD559646	CD559646
45	58	3.4	791	6	CD559647	CD559647

## ALIGNMENTS

RESULT 1  
CO918710  
LOCUS  
DEFINITION  
AGNCOURT 30488597 NIH MGC 145 Homo sapiens CDNA clone  
IMAGE:7211820 5', mRNA sequence.

ACCESSION  
CO918710  
VERSION  
CO918710.1 GI:51266406

KEYWORDS  
EST.  
Homo sapiens (human)

SOURCE  
Homo sapiens

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 694)

AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE  
Unpublished (1999)

JOURNAL  
Contact: Daniela S. Gerhard, Ph.D.

COMMENT  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-remail.nih.gov  
Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov  
plate: IRB15 row: c column: 10

High quality sequence stop: 489.

Location/Qualifiers  
1. 694

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:7211820"

/tissue\_type="mixed"

/lab\_host="DH10B"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XbaI-XhoI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRB1.prsSV.dat

ORIGIN a Note: this is a NIH\_MGC Library."

Query Match 40.3%; Score 678.8; DB 7; Length 694;  
 Best Local Similarity 98.6%; Pred. No. 1e-176;  
 Matches 663; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

157 GTGACTTCCCAAGTATGCTGGCAGAAATACCTCCAGAAATCTCTTGGATCTTATAG 216  
 2 GTGACTTCCCAAGTATGCTGGCAGAAATACCTCCAGAAATCTCTTGGATCTTATAG 61  
 217 TGAACACCCCACTTAATGAGCTTCTTCAATGCTTATGAGCGGCTGAGGCTGCA 276  
 62 TGAACACCCCACTTAATGAGCTTCTTCAATGCTTATGAGCGGCTGAGGCTGCA 121  
 277 TTTTCATCTCTTCCCTGCTGGAATGACACCGGCTGAGGACACCATAGGCGGTCA 336  
 122 TTTTCATCTCTTCCCTGCTGGAATGACACCGGCTGAGGACACCATAGGCGGTCA 181  
 337 TTAACCTGGTGTGTCAACAGCGTTTCTGCTGACAGTGCATTTCCCTGACCTTACC 396  
 182 TTAACCTGGTGTGTGTCAACAGCGTTTCTGCTGACAGTGCATTTCCCTGACCTTACC 241  
 397 TCATCAAGAAAGACTTGAATGTTTGGCTGCGCTTCTGCAAAATTTGAGTGCATCTGC 456  
 242 TCATCAAGAAAGACTTGAATGTTTGGCTGCGCTTCTGCAAAATTTGAGTGCATCTGC 301  
 457 ACATCCACATGATACCTGAGCTTCTTCTATGATGATGATGATGATGATGATGATGAT 516  
 302 ACATCCACATGATACCTGAGCTTCTTCTATGATGATGATGATGATGATGATGATGAT 361  
 517 TCTTCTTCAAGTCAAGAAAGAAAGTGAATTTCTACAGAAATCTGCTGCTGCTGCA 576  
 362 TCTTCTTCAAGTCAAGAAAGAAAGTGAATTTCTACAGAAATCTGCTGCTGCTGCA 421  
 577 GTGCTGGCATGTGAGCGCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 636  
 422 GTGCTGGCATGTGAGCGCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 481  
 637 GAATCCATGAGAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 696  
 482 GAATCCATGAGAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541  
 697 CATATGAGAAATCATCAATATATATATATATATATATATATATATATATATATAT 756  
 542 CATATGAGAAATCATCAATATATATATATATATATATATATATATATATATATAT 601  
 757 TGTGTGCTTCCAGGCTTCTCATATATATATATATATATATATATATATATATATAT 816  
 602 TGTGTGCTTCCAGGCTTCTCATATATATATATATATATATATATATATATATATAT 661  
 817 TATCCACAGAGGAGTCTGGGCTCAGCTGAAAA 849  
 662 TATCCACAGAGGAGTCTGGGCTCAGCTGAAAA 694

RESULT 2  
 AG145972 684 bp DNA linear GSS 08-JUN-2002  
 LOCUS AG145972  
 DEFINITION Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey  
 sequence.  
 ACCESSION AG145972  
 VERSION AG145972.1 GI:16675650  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
 TITLE Totoki, Y., Watanabe, H. and Sakaki, Y.  
 JOURNAL BAC end sequences of library RPECI-43  
 Unpublished

REFERENCE 2 (bases 1 to 684)  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
 TITLE Totoki, Y., Watanabe, H. and Sakaki, Y.  
 JOURNAL Direct Submission  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
 1-7-22 Suenhiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: chimpanseogsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/),  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170  
 Clones are derived from the chimpanzee BAC library RPECI-43. This BAC  
 end was generated during the R&D process and may have higher chance  
 of clone tracking errors.  
 PRIMERS  
 Sequencing: TU  
 LIBRARY  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.  
 Location/Qualifiers  
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 /db\_xref="taxon:9598"  
 /clone="RP43-007G22.TU"  
 /sex="male"  
 /cell\_type="lymphocytes"  
 /clone\_lib="RPECI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 38.3%; Score 644.4; DB 9; Length 684;  
 Best Local Similarity 98.2%; Pred. No. 3.7e-167;  
 Matches 662; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

531 AAAAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCTGCTGCTGCTGCTG 590  
 10 AAAAATCCGCGCTTCTTACAGAAATCTGATGCTGTGCTGCTGCTGCTGCTGCTG 69  
 591 ACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 650  
 70 ACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 129  
 651 TACAAAGAGGAGCACTGTTTAAATTTCAAAAAGCTTGTCTTACATATGTAATTC 710  
 130 TACAAAGAGGAGCACTGTTTAAATTTCAAAAAGCTTGTCTTACATATGTAATTC 189  
 711 ATCAAT 770  
 190 ATCAAT 249  
 771 GTCTTCAT 830  
 250 GTCTTCAT 309  
 831 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGCTATCTTGTGTTTCTTCC 890  
 310 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGCTATCTTGTGTTTCTTCC 369  
 891 TACAGATTTTATAGATCTATATCTATATATATATATATATATATATATATATATAT 950  
 370 TACAGATTTTATAGATCTATATCTATATATATATATATATATATATATATATATAT 429  
 951 AAGGTGATTTTATAGAAATCTTCTTATAGTATAGCAATATAGCTATGATTTG 1010  
 430 AAGGTGATTTTATAGAAATCTTCTTATAGTATAGCAATATAGCTATGATTTG 489  
 1011 CTTCCTTGTGTTTGGGGGAAGCCATTTGTTAAGCAAAAGATTAATTTGCTTATGAT 1070  
 490 CTTCCTTGTGTTTGGGGGAAGCCATTTGTTAAGCAAAAGATTAATTTGCTTATGAT 549  
 1071 TGTGTTTGTGCTGCTTACCAAACTACAGATTCATATTTGCTTCTTATATTTGGA 1130  
 550 TGTGTTTGTGCTGCTTACCAAACTACAGATTCATATTTGCTTCTTATATTTGGA 609

QY 1131 AT-AAAATGGGTATAGGGAGGTAAAGATGTTATTTCTTACTTATGATCAAAACCATGCT 1189  
| | | | |  
Db 610 ATAAAATGGGTATAGGGAGGTAAAGATGTTATTTCTTACTTATGATCAAAACCATGCT 669  
| | | | |  
QY 1190 TGATGTACCAAAA 1203  
| | | | |  
Db 670 TGATGTACCAAAA 683  
| | | | |  
RESULT 3  
CO18845/c 717 bp mRNA linear EST 16-AUG-2004  
LOCUS AGENCOURT 30698387 NIH MGC 145 Homo sapiens cDNA clone  
DEFINITION IMAGE:7211820 3', mRNA sequence.  
ACCESSION CO18845  
VERSION CO18845.1 GI:51266673  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS 1 (bases 1 to 717)  
TITLE NIH-MGC http://mgs.nci.nih.gov/  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: IRB15 row: C column: 10  
High quality sequence stop: 515.  
Location/Qualifiers  
1. 717  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:7211820"  
/issue\_type="mixed"  
/lab\_host="DH10B"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRB1-presv.dat  
a Note: this is a NIH-MGC Library."

ORIGIN  
Query Match 38.1%; Score 642.2; DB 7; Length 717;  
Best Local Similarity 98.4%; Pred. No. 1.5e-166;  
Matches 656; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
| | | | |  
QY 483 TTCTATGTGTGATCTGTACCAAGTACTTCTTCAAGTCAAGCAAAAGCAAGT 542  
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Db 669 TTTTATGGGTGATCTGTACCAAGTACTTCTTCAAGTCAAGCAAAAGCAAGT 610  
| | | | |  
QY 543 GAATTCACGAAACCTGATGCTGTGCTGCCAGTCTGGCATGTGAGCGTGTGATT 602  
| | | | |  
Db 609 GAATTCACGAAACCTGATGCTGTGCTGCCAGTCTGGCATGTGAGCGTGTGATT 550  
| | | | |  
QY 603 GTCAATGTGTACCCCTGTTGTCTCCGGTATGTGAATCATGAGAAATCAATGAGAG 662  
| | | | |

Db 549 GTCAATGTGTACCCCTGTTGTCTCCGGTATGTGAATCATGAGAAATCAATGAGAG 490  
| | | | |  
QY 663 CATCTTTTAAATTTTCACAAAGCTTGTCTTACACATATGTGAATCATCACTATATG 722  
| | | | |  
Db 489 CACTGTTTAAATTTTCACAAAGCTTGTCTTACACATATGTGAATCATCACTATATG 430  
| | | | |  
QY 723 ATAGTCAATTTTTCATAGCCGTTGCTGTGATCTGTGTGCTTCCAGGCTTCATCATTT 782  
| | | | |  
Db 429 ATAGTCAATTTTTCATAGCCGTTGCTGTGATCTGTGTGCTTCCAGGCTTCATCATTT 370  
| | | | |  
QY 783 ATGTGTATGTGTGAGAGAGTACGCCACTCTTACTATATCCACGAGAGTTCTGGGCTCAG 842  
| | | | |  
Db 369 ATGTGTATGTGTGAGAGAGTACGCCACTCTTACTATATCCACGAGAGTTCTGGGCTCAG 310  
| | | | |  
QY 843 CTGAAAACCTATTTTATATAGGGGTCACTCTGTTGTTTCTTCCCTACCACTTCTT 902  
| | | | |  
Db 309 CTGAAAACCTATTTTATATAGGGGTCACTCTGTTGTTTCTTCCCTACCACTTCTT 250  
| | | | |  
QY 903 AGGATCTATTACTTGAATGTGTGAGCAATTCGAATGCCGTGACGAAAGTTTGCAATT 962  
| | | | |  
Db 249 AGGATCTATTACTTGAATGTGTGAGCAATTCGAATGCCGTGAGCAAGTTTGCAATT 190  
| | | | |  
QY 963 TATACGAATCTTCTTGAAGTGAAGCAATAGCTGATGATTTGCTTCTTGTGTC 1022  
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Db 189 TATACGAATCTTCTTGAAGTGAAGCAATAGCTGATGATTTGCTTCTTGTGTC 130  
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QY 1023 TTTGGGGGAAGCCATGTTTAAAGCAAAAGATATAGCTTATGAAATGTGTTTGTGC 1082  
| | | | |  
Db 129 TTTGGGGGAAGCCATGTTTAAAGCAAAAGATATAGCTTATGAAATGTGTTTGTGC 70  
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QY 1083 CGTTACCCCAAACTACATATTCATATTTGCTTCTTATATTTGGAAAT-AAAGGGG 1141  
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Db 69 CGTTACCCCAAACTACATATTCATATTTGCTTCTTATATTTGGAAAT-AAAGGGG 10  
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QY 1142 ATAGGGGAG 1150  
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Db 9 ATAGGGGAG 1  
| | | | |

RESULT 4  
BF160725 772 bp mRNA linear EST 30-OCT-2000  
LOCUS 601769127F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',  
DEFINITION mRNA sequence.  
ACCESSION BF160725  
VERSION BF160725.1 GI:11040832  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS 1 (bases 1 to 772)  
TITLE NIH-MGC http://mgs.nci.nih.gov/  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LLAM9196 row: F column: 07  
High quality sequence stop: 634.  
Location/Qualifiers  
1. 772  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3988230"

/issue\_type="spontaneous tumor, metastatic to mammary.  
Stem cell origin."  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;  
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 24.7%; Score 415.8; DB 2; Length 772;  
Best Local Similarity 79.2%; Pred. No. 1.1e-103;  
Matches 544; Conservative 0; Mismatches 137; Indels 6; Gaps 4;

261 GGGCTGTGGGTGATCTTTCATCTTTCTCCCTGCTGTAAGAACCCGGTAGTG 320  
1 GGAAGTGAAGGCTCATCTCCATCTGTTCTGCTGTAAATGAACTCAGTTAGTG 60  
321 ACCACCATGCGGCTCAATTAATGTTGTTGTCACAGCGTTTCTGCTGACAGTGC 380  
61 ACCACCATGCGGCTCAATTAATGTTGTTGTCACAGCGTTTCTGCTGACAGTGC 120  
381 TTTGCTTGAAGCTCAATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 440  
121 TTTGCTTGAAGCTCAATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 179  
441 GTGAGTGCATGCTGACATCCATGTTACCTTCATCTTCTGTTGTTGTTGTTGTTG 500  
180 GTGAGTGCATGCTGACATCCATGTTACCTTCATCTTCTGTTGTTGTTGTTGTTG 239  
501 GTGACAGATACCTCAATCTTCTTCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCA 560  
240 GTGACAGATACCTCAATCTTCTTCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCA 299  
561 CATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620  
300 CATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359  
621 GTTGTCTCCCGGATGGAATCCATGAGAAATCAATGAGAGACGTTTAAATTTGAC 680  
360 GTTGTCTCCCGGATGGAATCCATGAGAAATCAATGAGAGACGTTTAAATTTGAC 419  
681 AAAGAGCTTGTCAATATGTAATATCAATCAATATATATATATATATATATATAT 740  
420 AAAGAGCTTGTCAATATGTAATATCAATCAATATATATATATATATATATATAT 479  
741 GCGGTGTGCTGATCTGTTGTTCTTCCAGTCTTCAATATATATATATATATATAT 800  
480 GCGGTGTGCTGATCTGTTGTTCTTCCAGTCTTCAATATATATATATATATATAT 539  
801 CTACGCGCATCTTAT 860  
540 TTTGCGCATCTTAT 598  
861 AATAGGAGTCA--TCTTGTGTTGTTCTTCCCTTACAGTCTTAAATATATATAT 917  
599 AATAGGATACAT 657  
918 AATGTGTGACAT 944  
658 TGTGTTGGGGGCTGCCAGAGCTGAT 684

RESULT 5  
A2554824 580 bp DNA linear GSS 20-NOV-2000  
LOCUS A2554824  
DEFINITION RPCI-23-211E13.TV RPCI-23 Mus musculus genomic clone  
ACCESSION RPCI-23-211E13, genomic survey sequence.  
VERSION A2554824  
KEYWORDS A2554824.1 GI:11234644  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

REFERENCE  
1 (bases 1 to 580)  
AUTHORS Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatman,S.,  
Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de  
Jong,P. and Fraser,C.M.  
TITLE Mouse BAC End Sequences from Library RPCI-23  
JOURNAL Unpublished (1999)  
COMMENT Other GSSs: RPCI-23-211E13.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
or from Resea ch Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end page:  
[http://www.igr.org/cdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.igr.org/cdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 211 row: E column: 13  
Seq primer: 17  
Class: BAC ends.

FEATURES  
source location/Qualifiers

1..580  
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/clone="RPCI-23-211E13"  
/sex="Female"  
/lab\_host="DH10B"  
/clone\_lib="RPCI-23"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1:  
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Site  
selected DNA was cloned into the pBAC3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 21.0%; Score 354.2; DB 8; Length 580;  
Best Local Similarity 78.3%; Pred. No. 1.2e-86;  
Matches 450; Conservative 0; Mismatches 123; Indels 2; Gaps 2;

556 AACTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615  
1 AATTCATGCAAGTGTCTGCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 59  
616 CCTGTGTGTCTCCGGTATGGAATCCATGAGAAATCAATGAGAGCACTGTTTAAT 675  
60 CCTGTGTGTGTCTGAGTATGGAATATAGCAAGAAATCAATGAGAGCAAGTCTTAAT 119  
676 TTCAAGAGAGTGTCTTACATATATGAAATATCAATATATATATATATATATATAT 735  
120 TTCAATTAAGAACTTGCGCATGATCTGTCGAGATATCAATATATATATATATATAT 179  
736 TCATAGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795  
180 TCATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239  
796 AGAGCTACGCACTCTTACTATCCACAGAGATTCTGGGCTCAGCTGAAAACCTAT 855  
240 GGAAGTTTCGCACTCTTACTATCCACAGAGATTCTGGGCAACAATGAAAATCTTT 299  
856 TTTTATAGGGGATCACTCTGTTGTTCTTCCCTTACAGTCTTAAATATATATATAT 915  
300 TCTTTATAGGATCAAT 359  
916 TGAATGTTGACGATTCATATGCTGTACAGAGAGTTGACATTTTATACGAATCT 975

Db	360	TGTATGTTGTGGCACATTCGACAGACTGTAAAAAGAAAGTTGATTTTACATGAAATCC	419		
Qy	976	TCTTGAAGTGAACAGCAATTAAGTCTGTATGATTGCTTCTTTGCTTTGGGGAGACC	1039		
Db	420	TATTGAGCAACAACGACATCAGCTCTGTGATTGCTCTTTTGTCTTTGGAGGAGCC	479		
Qy	1036	ATTGTTTAAAGAAAAGATTAATGGCTATAGAAATTTGTGTCCTTATGCCACAA	1095		
Db	480	ATTGGATTAAAGAAAAGATTTGCAACATGTGGAAATGGCTTTATGACATTAGCA-AGA	538		
Qy	1096	CTACAGTATTCATATTGCTTCTTATATTGGGA	1130		
Db	539	TTACCATATCTTTCTTCTCTGTTGGAAATTGAA	573		
RESULT 6	A0888495	456 bp	DNA	linear	GSS 10-NOV-1999
LOCUS	A0888495	HS_3162_B1_B01_MR	CIT	Approved Human Genomic Sperm Library D Homo	
DEFINITION		sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey			
ACCESSION	A0888495				
VERSION	A0888495.1	GI:6344685			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 456)			
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17)	9739-9744	(1999)	
MEDLINE	99380589				
PUBMED	10449764				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3162 Row: D Column: 1 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 456.				
FEATURES	source	location/Qualifiers			
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		/mol_type="genomic DNA"			
		/db_xref="taxon:9606"			
		/clone="Plate=3162 Col=1 Row=D"			
		/sex="male"			
		/clone_lib="CIT Approved Human Genomic Sperm Library D"			
		/note="Organ: sperm; Vector: pbeloBAC11; BAC clones in E-Coli DH10B"			
ORIGIN					
Query Match	20.1%;	Score 338;	DB 8;	Length 456;	
Best Local Similarity	97.3%;	Pred. No. 3.6e-82;			
Matches 364;	Conservative 0;	Mismatches 7;	Indels 3;	Gaps 2;	
Qy	549	TACAGAAAATGCATGCTGTGGCTGCCAGTCTGCGATGTGAGACGCTGTGATTGTATT	608		
Db	1	TACAGAAAATGCATGCTGTGGCTGCCAGTCTGCGATGTGAGACGCTGTGATTGTATT	60		
Qy	609	GTGTATCCCCCTGTGTCTCCCGGTATGGAATTCATAGCAATACATAGAGACACTGT	668		

Db	61	GTGGTACCCCTGGTGTCTCTCCGGTATAGGAATTCATAGAAGATATCAGAGACACTCT	120
Qy	669	TTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATCATCAACTATATGATGTC	728
Db	121	TTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATCATCAACTATATGATGTC	180
Qy	729	ATTTTGTGCATAGCCGTTCGTGTGATTCCTGTGGATCTTCCAGGTCTTCATCATTTATGTTG	788
Db	181	ATTTTGTGCATAGCCGTTCGTGTGATTCCTGTGGATCTTCCAGGTCTTCATCATTTATGTTG	240
Qy	789	ATGNGCAGAAAGCTACGCACTCTTTACTATATCCACAGAGAGTCTGGGGCTCAGCTGAAA	848
Db	241	ATGNGCAGAAAGCTACGCACTCTTTACTATATCCACAGAGAGTCTGGGGCTCAGCTGAAA	300
Qy	849	AACCTATTTTATATAGAGGATCATCTTGTGTTTGTTCCTTCCCTACAGTCTTTAGGATC	908
Db	301	AAACCTATTTTATATAGAGGATCATCTTGTGTTTGTTCCTTCCCTACAGTCTTTAGGATC	357
Qy	909	TATTACTTGAATGT 922	
Db	358	TATTACTTGAATGT 371	
RESULT 7			
EX952455			
LOCUS	EX952455	678 bp mRNA linear	EST 01-MAR-2004
DEFINITION	DKFZp781N17197.r1.781 (synonym: h1cc4) Homo sapiens cDNA clone		
ACCESSION	DKFZp781N17197.5', mRNA sequence.		
VERSION	EX952455		
KEYWORDS	EX952455.1 GI:43429371		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 678)		
JOURNAL	Wambuit,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.		
COMMENT	EST (Wambuit,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.) Unpublished (2003)		
	Contact: MIPS		
	IngoIsaetler Landstr.1, D-85764 Neuherberg, Germany		
	This is the 5' sequence of the clone insert		
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;		
	Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.		
	No sl sequence available.		
	This clone (DKFZp781N17197) is available at the RZPD in Berlin.		
	Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..678		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="DKFZp781N17197"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/clone_1ib="781 (synonym: h1cc4)"		
	/note="Vector: pSport1_sfi, Site_1: SfiIA, Site_2: SfiIB, cDNA-collection"		
ORIGIN			
Query Match	19.3%;	Score 325.8;	DB 5; Length 678;
Best Local Similarity	99.1%;	Pred. No. 1e-78;	
Matches 327;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	153	AAATGACATTTCCCAAGTATAGCTTGACACAAATCTCCAGAAATCTCTTGCAATCCT	212
Db	349	ACAGGATACCTTCCCAAGTATAGCTTGACACAAATCTCCAGAAATCTCTTGCAATCCT	408

QY 213 ATAGTACACCCCACTTAATCAGCCCTCTCATAGTCTTATTTGGCGGCTGTGGGT 272  
|  
|  
|  
Db 409 ATAGTACACCCCACTTAATCAGCCCTCTCATAGTCTTATTTGGCGGCTGTGGGT 468  
|  
|  
|  
QY 273 GTCATTTCCATTTCTTTCTCTCTGTGAAATGACAACCCGGTCACTGACACCATGGC 332  
|  
|  
|  
Db 469 GTCATTTCCATTTCTTTCTCTCTGTGAAATGACAACCCGGTCACTGACACCATGGC 528  
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|  
|  
QY 333 GTCATTTCCATTTCTTTCTCTCTGTGAAATGACAACCCGGTCACTGACACCATGGC 392  
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|  
|  
Db 529 GTCATTTCCATTTCTTTCTCTCTGTGAAATGACAACCCGGTCACTGACACCATGGC 588  
|  
|  
|  
QY 393 TACCTCATCAGAAGAAGCTTGATGTTGGGCTGCTCTGCAAAATTTGTAGTGCATG 452  
|  
|  
|  
Db 589 TACCTCATCAGAAGAAGCTTGATGTTGGGCTGCTCTGCAAAATTTGTAGTGCATG 648  
|  
|  
|  
QY 453 CTGCACATCCACATGTACTCTCACGTTCTTA 482  
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|  
|  
Db 649 CTGCACATCCACATGTACTCTCACGTTCTTA 678  
|  
|  
|  
RESULT 8  
CV329473 306 bp mRNA linear EST 24-SEP-2004  
LOCUS CV329473 IL2-UM0076-180500-088-H05 UM0076 Homo sapiens cDNA, mRNA sequence.  
DEFINITION CV329473  
ACCESSION CV329473 GI:52652687  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 306)  
Dias, N.E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. http://www.ludwig.org.br.  
Location/Qualifiers  
1..306  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_id="UM0076"  
/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORFESTS PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
ORIGIN  
Query Match 16.7%; Score 280.6; DB 7; Length 306;  
Best Local Similarity 98.0%; Pred. No. 2.7e-66;  
Matches 294; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1285 CCAAGTGTGTAATCCACCTGAGTTGCAATATTATATTTCCAGTACAGATGTC 1344  
|  
|  
|  
Db 8 CCAAGTGTGTAATCCACCTGAGTTGCAATATTATTTCCAGTACAGATGTC 67  
|  
|  
|  
QY 1345 TGTGTGCCCCATGAAAGCAACATAGTTTAAAGATTATTAAGTTTCAATAGCTCATTC 1404  
|  
|  
|  
Db 68 TGTGTGCCCCATGAAAGCAACATAGTTTAAAGATTT-AAAGTTTATTAAGTTCATTC 126  
|  
|  
|  
QY 1405 TAAAGTTCTCTGTTGAAGCATGTCCTTGTAGTTTGTGAATGCACTGAGACCTTAACT 1464  
|  
|  
|  
Db 127 TAAAGTTCTCTGTTGAAGCATGTCCTTGTAGTTTGTGAATGCACTGAGACCTTAACT 186  
|  
|  
|  
QY 1465 CTTTTCATCCCACTTCCACATAGTAATTAATTCTGGCCACACCCAGCTCCAAAGACA 1524  
|  
|  
|  
Db 187 CTTTTCATCCCACTTCCACATAGTAATTAATTCTGGCCACACCCAGCTCCAAAGACA 246  
|  
|  
|  
QY 1525 CAAACTCTCTTCTGCTTAAACAGTTAGATGTCCTCATCTCATGCTGATTAATAAACT 1584  
|  
|  
|  
Db 247 CAAACTCTCTTCTGCTTAAACAGTTAGATGTCCTCATCTCATGCTGATTAATAAACT 306  
|  
|  
|  
RESULT 9  
BG862323 646 bp mRNA linear EST 29-MAY-2001  
LOCUS BG862323 602796201P1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',  
DEFINITION BG862323  
ACCESSION BG862323 GI:14212861  
VERSION  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 646)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Purth  
Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM10828 row: b column: 01  
High quality sequence stop: 644.  
Location/Qualifiers  
1..646  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="NMRI"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4917024"  
/tissue="IMAGE:4917024"  
/dev\_stage="tumor, gross tissue"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP Mam4"  
/note="Organ: mammary; Vector: PCMV-SPORE6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Priscilla Purth,  
NIH Reference for transgenic model: Li et al., Cell Growth  
and Differentiation 7, 3-11 (1996)."  
ORIGIN  
Query Match 14.1%; Score 237.2; DB 4; Length 646;  
Best Local Similarity 79.4%; Pred. No. 3.8e-54;  
Matches 281; Conservative 0; Mismatches 73; Indels 0; Gaps 0;



OY		157	GTGACTTCCCAAGTATGCCTGGCGACAATAACCTCCAGAAATTCCTTGCCATTGCTAATAG	216
Db		293	GTAATGTTGAAGAATGATGATATATAACTTCGAGATATCTCTTGACCTTAATAC	352
OY		217	TGACACCCCACCTTAATACAGCCTCTCATCTTATAGTCTTAATTTGGCGGGCTGTGGGTCTCA	276
Db		353	TGGCACACACACTTAACATGGAATTTACTCATATGAGTCTCATTTGGABAGACTGGTAGGCCCTCA	412
OY		277	TTTTCAATCTTTTTCCTCCTGTGTGAATAATGACACCCTGGTCAAGTCCATGGCGGTCA	336
Db		413	TCTCCATCCGGTCTTCTTGCTGTGGAAAATGAACTCAACGTTTCAAGTGACACACATGGCTGTCA	472
OY		337	TTAACCTGGTGGTGGTCCACAGCGTCTTTCTGTCTGACAGTGCATTTTGGCTTGACTTAC	396
Db		473	TCAACCTGTGGTGGTTCATGAGGGGTCTTCTCATCTGACAGGTGCTTTCGGCTTGGATAC	532
OY		397	TCATCAAGAGAAGCTTGATGTTTGGAGCTGCCCTTCTTGCAAAATTTTGAAGTGCATGCTAC	456
Db		533	TCATCAAGAGGACTTGGAGCTTGGATTTACCTTCTTGCAAAATTTTGAAGTGCATGCTTAC	592
OY		457	ACATTCACATGTACTCTCAAGTTCCTAATCTATGTGTGATATCTGTGTCAACAGAT	510
Db		593	ATATTCACATGTACTCTCAAGTTCCTTCTTCTAAGTGTGTACTGATCATGAT	646
RESULT	10			
	CD699779	499 bp	mRNA	linear EST 25-JUN-2003
LOCUS	EST16303	human nasopharynx	Homo sapiens cDNA,	mRNA sequence.
DEFINITION	CD699779			
ACCESSION	CD699779.1	GI:32229387		
VERSION				
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 499)			
AUTHORS	Liu,X.-Q., Zhou,Y., Zhang,J.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gszsum.edu.cn. Location/Qualifiers			
FEATURES				
source	1..499			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/issue_type="normal nasopharynx"			
	/clone_lib="human nasopharynx"			
	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
Query Match	12.1%;	Score 203;	DB 6;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 1.le-44;		
Matches 203;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
OY		157	GTGACTTCCCAAGTATGCCTGGCGACAATAACCTCCAGAAATTCCTTGCCATTGCTAATAG	216
Db		297	GTGACTTCCCAAGTATGCCTGGCGACAATAACCTCCAGAAATTCCTTGCCATTGCTAATAG	356
OY		217	TGACACCCCACCTTAATACAGCCTCTCATCTTATAGTCTTAATTTGGCGGGCTGTGGGTCTCA	276
Db		357	TGACACCCCACCTTAATACAGCCTCTCATCTTATAGTCTTAATTTGGCGGGCTGTGGGTCTCA	416
OY		277	TTTTCAATCTTTTCTCCTGTGTGAATAATGACACCCTGGTCAAGTCCATGGCGGTCA	336

Db	417	TTTCATCTTCTTCTCCTGGTGAAATGAACACC GGTCAGTAGCACCACTGCGGTCA	476
Oy	337	TTAACTTGSGTGGTCCACAGC	359
Db	477	TTAATTGGTGGTCCACAGC	499
RESULT 11			
BGI45683		478 bp	mRNA linear EST 01-FEB-2001
LOCUS			
DEFINITION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			

```

BGI45683
mac33c07.y1 Soares mouse 3NbMs Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.
BGI45683
BGI45683.1 GI:12649019
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 478)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapdb-tdmail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:1499380
Seq primer: -40RP from Gibco
High quality sequence stop: 392.
Location/Qualifiers
1..478
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4001652"
/bex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_id="Soares mouse 3NBMS"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGTAAGTGGAGCGGCCGCCTGTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Benito Soares and W.Fatima Bernaldo."

```

Query Match 11.8%; Score 199; DB 4; Length 478;  
Best Local Similarity 69.9%; Pred. No. 1,4e-43;  
Matches 343; Conservative 0; Mismatches 135; Indels 13; Gaps 5;

OY	860	TATAGGGGTCATCTTGTGTTCCTTCCCTACCACTTCTTATGAGATCTATTAAGTGA	919
DB	1	TATAGTATCATATTAATTGTGT-TCTCCCTACCACTTCTTATGAGATTAATTAATTGTA	59
OY	920	TGTTGTGACCCATTCACATGCCCTGTAGACACAAGTGTGATTTATAACCAAACTCTT	979
DB	60	TGTTGTGACCATTCACCAAGAGCTGTAAAAACAAGTTGACATTTTACATGAAAATCCATTT	119
OY	980	GAGGTATACAGCAATTAGTGTGATATGATTTGTCTTCTTGTCTTTGGGGAAGCCATYTG	1039
DB	120	GAGACAAACAGCCATCAGCTGCTGTATTTGCTGCTTTTGTCTTTGGAGAAGCCATTTG	179
OY	1040	GTTTATGCAAAAGATTAATTGGCTTATGGAATGTGTGTCGCGTTAGCCACAACACTAC	1099

Db 180 GGTAAAGCAAAAGATTGTCAGATGTCAGATTGCTTATGTCATTAGCCA-AGATTAC 238  
QY 1100 AGTATTCATATTTGTTCTTCTTATATTTGGGAATTAAGGATPAGGAGGTAAGANG 1159  
Db 239 CATATTTCTTTTCTTCTGTTGGGAATTTGGATACGA-----AGAGGCTTAAGATG 289  
QY 1160 GATATTCATTTCTTGTATCAAAACCATGCTTGTATGACCAAAAGAGCTATTA 1219  
Db 290 ATTTTCATTTGCTTCAATGAAACCTGCTGGCCCAACC-AAACAAAGGAATTAAGAG 348  
QY 1220 TGGAAAGCCCTCATTTGATGCTTATGGAATCCCTCCATCTGTAGTGATGCGCTAC 1279  
Db 349 TGCCAAAGCTCTTACTACGCTGATTAATAATACCTGTTGTGGGA-AGGTGTCATGC 407  
QY 1280 AAAGACAGTGTGTTGAATCCACCTGAGTTGCAATATTATTTCCAGTACAGA 1339  
Db 408 AAAGATGATGTTGTAGGAACCTATAGGAATTCCTGATTTGATTTTTCACATACA 467  
QY 1340 ATGCTGTGTG 1350  
Db 468 GTGTCTACTTG 478

RESULT 12  
BG461295 649 bp mRNA linear EST 21-APR-2001  
LOCUS RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
DEFINITION BG461295  
ACCESSION BG461295  
VERSION BG461295.1 GI:13749801  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 649)  
Harrington,J.U., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,  
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,  
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,  
Offenbacher,J., Danzig,J. and Ducar,M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
JOURNAL 21227151  
MEDLINE 11329013  
PUBMED  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com.  
Location/Qualifiers  
FEATURES  
source 1..649  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Athersys RAGE Library"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

ORIGIN  
Query Match 10.7%; Score 181; DB 4; Length 649;  
Best Local Similarity 74.1%; Pred. No. 1.5e-38;  
Matches 355; Conservative 0; Mismatches 50; Indels 74; Gaps 7;  
QY 157 GTGACTTCCCAAGTATGCTGGCCCAATACTCCAGGAATTCCTTGGCATCTTAG 216  
Db 108 GTGACTTCCCAAGTATGCTGGCCCAATACTCTTATCTTAG 151

QY 217 TGACACCCCACTTAATCAGCCTTACTTATAGTCTTATTGGCGGGCTGGTGTCA 276  
Db 152 TGACACCCCACTTAATCAGCCTTACTTATAGTCTTATTGGCGGGCTGGTGTCA 211  
QY 277 TTTTCATTTCTTTCTCTCTGTTGAAAATGACAACCCGGTCAGTGACCATGCGGTCA 336  
Db 212 TTTTCATTTCTTTCTCTCTGTTGAAAATGACAACCCGGTCAGTGACCATGCGGTCA 254  
QY 337 TTAATCTGTGTGTGTCACAGCGTTTCTGTCGACAGTG-CGATTTGCTGACCTAC 395  
Db 255 TTAATCTGTGTGTGTCACAGCGTTTCTGTCGACAGTGCCATTTGCTGACCTAC 314  
QY 336 CTGATCAAGAAAGATGTGATGTTGGGCTGCGCTTCTGCAATTTGTAGTGCCATGCTG 455  
Db 315 C-----CTTTGGGCTGCGCTTCTGCAATTTGTAGTGCCATGCTG 356  
QY 456 CACATCCACATGATCTGACGTTCTT-ATTCTATGTGTGATCTGTCACCAATGATCT 514  
Db 357 AACATTTCAATGTACTGACGATCTTAATGCGCTGATCTTCCGCGCGGAT---- 412  
QY 515 CATCTTCTTCAAGTCAAGCAAGATGGAATTCACAGAAACATGATGCTGTGCTGC 574  
Db 413 -----CAAGACAAAGCGACTT-TACAGATGCTGCGCCCGAGGTTGC 455  
QY 575 CAGTCTGCGCATGTGAGACGCTGTGATTTGTCAATGTGTGACCCCTGTTGTCTCCGGT 633  
Db 456 CAGACTGCGCATGTGAGACGCTGTGATTTGTCAATGTGTGACCCCGCGGCTTTCCGGGT 514

RESULT 13  
BG221739 283 bp mRNA linear EST 21-APR-2001  
LOCUS RST41554 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
DEFINITION BG221739  
ACCESSION BG221739  
VERSION BG221739.1 GI:13747760  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 283)  
Harrington,J.U., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,  
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,  
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,  
Offenbacher,J., Danzig,J. and Ducar,M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
JOURNAL 21227151  
MEDLINE 11329013  
PUBMED  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com  
High quality sequence stop: 233.  
Location/Qualifiers  
FEATURES  
source 1..283  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Athersys RAGE Library"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 9.6%; Score 162; DB 4; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-33;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 GTGACCTTCCAGATGATGCTGGCCACATACCTCAGGAATTCCTTGGCATCTTAG 216  
 Db 122 GTGACCTTCCAGATGATGCTGGCCACATACCTCAGGAATTCCTTGGCATCTTAG 181

Qy 217 TGACACCCCACTTATGAGCTCTTACTTATGCTTATTTGGCGGCTGGTGGTCA 276  
 Db 182 TGACACCCCACTTATGAGCTCTTACTTATGCTTATTTGGCGGCTGGTGGTCA 241

Qy 277 TTTCATTTCTTCTCTGCTGTAATGAAACACCGCTAG 318  
 Db 242 TTTCATTTCTTCTCTGCTGTAATGAAACACCGCTAG 283

RESULT 14  
 AK041317  
 LOCUS  
 DEFINITION  
 AK041317 2774 bp mRNA linear HTC 03-APR-2004  
 Mus musculus adult male aorta and vein cDNA, RIKEN full-length  
 enriched library, clone:A530099J19 product:hypothetical  
 Rhodopsin-like GPCR superfamily containing protein, full insert  
 sequence.  
 AK041317  
 AK041317.1 GI:26334372  
 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

REFERENCE  
 AUTHORS  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)

JOURNAL  
 MEDLINE  
 PUBMED  
 99279253  
 10349636

REFERENCE  
 AUTHORS  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Kono, H., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL  
 MEDLINE  
 PUBMED  
 20499374  
 11042159

REFERENCE  
 AUTHORS  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL  
 MEDLINE  
 PUBMED  
 20530913  
 11076861

REFERENCE  
 AUTHORS  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

JOURNAL  
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 PUBMED  
 20530913  
 11076861

REFERENCE  
 AUTHORS  
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

JOURNAL  
 MEDLINE  
 PUBMED  
 12042159  
 12042159

REFERENCE  
 AUTHORS  
 6 Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 Kanagawa 230-0045, Japan (E-mail: genome-res@isc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
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VERSION AJ455645.1 GI:20265741
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            1 (bases 1 to 834)
REFERENCE Buerstedde, J.M.
            Gallus gallus bursal lymphocyte EST
            Unpublished (2002)
COMMENT Contact: Buerstedde JM
            Cellular Immunology
            Heinrich-Pette-Institute
            Martinistr. 52, 20251 Hamburg, Germany
            Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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FEATURES
source

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## ORIGIN

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Query Match      8 4%; Score 142; DB 1; Length 834;
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Matches 225; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

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QY 526 AGTGAAAGACAAAGTGAATTCTACAGAAAATGCATGCTGTGTGCCA 576
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Job time : 6093.21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:41:45 ; Search time 1214.69 Seconds  
(without alignments)  
9104.583 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 731250 seqs, 3283620254 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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Publication No. US20030087249A1  
GENERAL INFORMATION:  
APPLICANT: GLICKSMAN, MARIA ALEXANDRA  
TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED  
FILE OF INVENTION: RECEPTOR AND USBS THEREFOR  
FILE REFERENCE: MP12001-021P1RCP1M  
CURRENT APPLICATION NUMBER: US/10/085,233B  
CURRENT FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: 60/272,677  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
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FEATURE:  
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LOCATION: (147) ... (1085)  
OTHER INFORMATION: n at position 1384 can be any  
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US-10-085-233B-1

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DB 1141 TATAGGGAGTGAAGATGATTTTCACTTATGATCAAAACCATGCTTATGATGCCA 1200  
QY 1201 AAACAAAGGATCTATTAATGCAAGAGCCCTCATTTAGTCTTATGAGGATCCCTCCAT 1260  
DB 1201 AAACAAAGGATCTATTAATGCAAGAGCCCTCATTTAGTCTTATGAGGATCCCTCCAT 1260  
QY 1261 CTCTGATGATGAGCCGTAACAAAGACCAAGTGTGTAATCCACTGAGTGTGAATATTA 1320  
DB 1261 CTCTGATGATGAGCCGTAACAAAGACCAAGTGTGTAATCCACTGAGTGTGAATATTA 1320  
QY 1321 CATTTATTTTCCAGTACGAATGCTGATGAGCCCAATGAAGAAACATAGTTTAAAGAT 1380  
DB 1321 CATTTATTTTCCAGTACGAATGCTGATGAGCCCAATGAAGAAACATAGTTTAAAGAT 1380  
QY 1381 TTTNAGATTTCAATTAAGTCTATTAAGTCTTCTGTTGAAGCATGATCTTATGATTT 1440  
DB 1381 TTTNAGATTTCAATTAAGTCTATTAAGTCTTCTGTTGAAGCATGATCTTATGATTT 1440  
QY 1441 TGGACTGAATCTGACACTTTTATGCTTATTTTCAATCCCACTTACCAATGATTAATTTCT 1500  
DB 1441 TGGACTGAATCTGACACTTTTATGCTTATTTTCAATCCCACTTACCAATGATTAATTTCT 1500  
QY 1501 GGGCACCACCCAGCTCCAAAGACAAACCTCTCTTCTGCTAACAGATTAAGTCCCAT 1560  
DB 1501 GGGCACCACCCAGCTCCAAAGACAAACCTCTCTTCTGCTAACAGATTAAGTCCCAT 1560  
QY 1561 TCATCTCATGCTGCTGATTAATACTGATTAAGGGAGGAATGATTAATAATTTTCTAGGG 1620  
DB 1561 TCATCTCATGCTGCTGATTAATACTGATTAAGGGAGGAATGATTAATAATTTTCTAGGG 1620  
QY 1621 TATCATTAATCTGCTGATGAAGATGATGCTGATGATGCTGATGATGATGATGATG 1680  
DB 1621 TATCATTAATCTGCTGATGAAGATGATGCTGATGATGCTGATGATGATGATGATG 1680  
QY 1681 GCCG 1684  
DB 1681 GCCG 1684  
RESULT 2  
US-09-782-974C-81  
; Sequence 81, Application US/09782974C  
; Publication No. US20030082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor  
; FILE REFERENCE: 411USPHRM311  
; CURRENT APPLICATION NUMBER: US/09/782,974C  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 09/714,449  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28



PRIOR APPLICATION NUMBER: 60/185,554  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/186,530  
PRIOR FILING DATE: 2000-03-02  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 81  
LENGTH: 2525  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-782-974C-81

Query Match 87.4%; Score 1472.6; DB 10; Length 2525;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 153 AATGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGGAATTCCTTGGCATCT 212  
DB 9 AAGGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGGAATTCCTTGGCATCT 68  
QY 213 ATAGTGACCCCACTTATATGAGCTTCACTTATATGCTTATTTGGCGGGCTGGTGGT 272  
DB 69 ATAGTGACCCCACTTATATGAGCTTCACTTATATGAGCTTATTTGGCGGGCTGGTGGT 128  
QY 273 GTCAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 332  
DB 129 GTCAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 188  
QY 333 GTCAATTTCTTGGTGGTGGTCCAGAGCTTTTCTGCTGACAGTSCATTTCCGTTGAC 392  
DB 189 GTCAATTTCTTGGTGGTGGTCCAGAGCTTTTCTGCTGACAGTSCATTTCCGTTGAC 248  
QY 393 TACCTCATCAAGAAAGCTTGAATTTTGGGCTGGCCCTTCTGCAATTTTGTGATGTCATG 452  
DB 249 TACCTCATCAAGAAAGCTTGAATTTTGGGCTGGCCCTTCTGCAATTTTGTGATGTCATG 308  
QY 453 CTGCAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 512  
DB 309 CTGCAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 368  
QY 513 CTCAATTTCTTCAAGTGAAGAACCAAGTGAATTTCTACAGAAATCTGATGCTGGT 572  
DB 369 CTCAATTTCTTCAAGTGAAGAACCAAGTGAATTTCTACAGAAATCTGATGCTGGT 428  
QY 573 GCCAGTGTGCTGATGAGAGCTGGTGAATTTGATGATGATGATGATGATGATGATGATG 632  
DB 429 GCCAGTGTGCTGATGAGAGCTGGTGAATTTGATGATGATGATGATGATGATGATGATG 488  
QY 633 TATGGAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 692  
DB 489 TATGGAATTTCCATTTCTTCTCTGCTGGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 548  
QY 693 TACATATGTAAGAAATCATCACTATATGATGATGATGATGATGATGATGATGATGATG 752  
DB 549 TACATATGTAAGAAATCATCACTATATGATGATGATGATGATGATGATGATGATGATG 608  
QY 753 ATTCGTGTGCTTCCAGTCTTCACTATATGATGATGATGATGATGATGATGATGATGATG 812  
DB 609 ATTCGTGTGCTTCCAGTCTTCACTATATGATGATGATGATGATGATGATGATGATGATG 668  
QY 813 TTACTATTTCCCAAGAGTCTTGGGCTGAGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 872  
DB 669 TTACTATTTCCCAAGAGTCTTGGGCTGAGTGAATAAGAACCCGGTCAAGTACCACTTGGCG 728  
QY 873 CTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 932  
DB 729 CTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 788  
QY 933 TCCATATGCTGTAAGAGAGTGGTGAATTTTATATGAAATCTTCTGATGTAACAGCA 992  
DB 789 TCCATATGCTGTAAGAGAGTGGTGAATTTTATATGAAATCTTCTGATGTAACAGCA 848

QY 993 ATTAGCTGTATGATTTGCTTCTCTTGTCTTGGGGGAAGCCATTTGTTAAGCAAG 1052  
DB 849 ATTAGCTGTATGATTTGCTTCTCTTGTCTTGGGGGAAGCCATTTGTTAAGCAAG 908  
QY 1053 ATTAATGCTGTATGATTTGTTGTTGCTTGGGAGTGAAGCAAGTATGATTTATTT 1112  
DB 909 ATTAATGCTGTATGATTTGTTGTTGCTTGGGAGTGAAGCAAGTATGATTTATTT 968  
QY 1113 GCTTCTTATATTTGGGAAT-AAAATGGTATAGGGGAGTGAAGTATGATTTATTTAC 1171  
DB 969 GCTTCTTATATTTGGGAATTAATAATGGTATAGGGGAGTGAAGTATGATTTATTTAC 1028  
QY 1172 TTGATCAAAACCAAGCTTGAATGACCAAAACCAAGTATGATTTATTTATTTATTT 1231  
DB 1029 TTGATCAAAACCAAGCTTGAATGACCAAAACCAAGTATGATTTATTTATTTATTT 1088  
QY 1232 CATTTGATCTTATGAGATCCCTTCCATCTGATGATGATGATGATGATGATGATGATG 1291  
DB 1089 CATTTGATCTTATGAGATCCCTTCCATCTGATGATGATGATGATGATGATGATGATG 1148  
QY 1292 TGTGATTCACCTGAGTGGCAATATTTATTTTCCAGTACAGATGCTGTGTGG 1351  
DB 1149 TGTGATTCACCTGAGTGGCAATATTTATTTTCCAGTACAGATGCTGTGTGTGG 1208  
QY 1352 CCCATGAAGCAAGTATGATTTTAAAGTTTTAAAGTATGATTTATTTATTTATTTATTT 1411  
DB 1209 CCCATGAAGCAAGTATGATTTTAAAGTTTTAAAGTATGATTTATTTATTTATTTATTT 1267  
QY 1412 CTCTGTTTGAAGATGCTCTTCTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1471  
DB 1268 CTCTGTTTGAAGATGCTCTTCTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1327  
QY 1472 TCCCATTTCAACATGATGATTAATAATTTCTGGCCACCAAGCTTCAAGACCAAACTC 1531  
DB 1328 TCCCATTTCAACATGATGATTAATAATTTCTGGCCACCAAGCTTCAAGACCAAACTC 1387  
QY 1532 TCCCTTGGCTTACCGGTTAATGATGCTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1591  
DB 1388 TCCCTTGGCTTACCGGTTAATGATGCTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1447  
QY 1592 GGAGAGATGATTTTAAATTTTCTAGGATATCAATCTGATGAGAGTATCTGTCT 1651  
DB 1448 GGAGAGATGATTTTAAATTTTCTAGGATATCAATCTGATGAGAGTATCTGTCT 1507  
QY 1652 AGA 1654  
DB 1508 AGA 1510

## RESULT 3

US-10-467-492A-81  
Sequence 81, Application US/10467492A  
Publication No. US20050069976A1  
GENERAL INFORMATION:  
APPLICANT: Pharmacia & Upjohn Company  
APPLICANT: Vogel, Gabriel  
APPLICANT: Land, Peter  
APPLICANT: Wood, Linda S.  
APPLICANT: Parodi, Luis A.  
TITLE OF INVENTION: Novel G Protein Coupled Receptor  
FILE REFERENCE: 0411PFRM313  
CURRENT APPLICATION NUMBER: US/10/467,492A  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 81  
LENGTH: 2525  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-467-492A-81

Query Match 87.4%; Score 1472.6; DB 21; Length 2525;  
Best Local Similarity 99.6%; Pred. No. 0;



Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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QY 153 AAAAGTACTTCCCAAGTATGCTGGGCCAATACTCCAGGATTTCTCTGGGATCTT 212
Db 9 AAGAGTACTTCCCAAGTATGCTGGGCCAATACTCCAGGATTTCTCTGGGATCTT 68
QY 213 ATAGTGAACCCCACTTAATGAGCTCTAATCTTATGAGTCTTATTTGGCGGGCTGGTGG 272
Db 69 ATAGTGAACCCCACTTAATGAGCTCTAATCTTATGAGTCTTATTTGGCGGGCTGGTGG 128
QY 273 GTCAATTCATCTTTTCTCTGCTGAGAAAAGAAACCCGGTCAGTACCAACCATGCGG 332
Db 129 GTCAATTCATCTTTTCTCTGCTGAGAAAAGAAACCCGGTCAGTACCAACCATGCGG 188
QY 333 GTCAATTCATCTTTGCTGCTGAGGATTTTCTGCTGAGAGGCCATTTGGCTTAC 392
Db 189 GTCAATTCATCTTTGCTGCTGAGGATTTTCTGCTGAGAGGCCATTTGGCTTAC 248
QY 393 TACCTCATCAAGAGACTTGGATGTTGGGCTGCTGCTGCAATTTTGTAGTGCATG 452
Db 249 TACCTCATCAAGAGACTTGGATGTTGGGCTGCTGCTGCAATTTTGTAGTGCATG 308
QY 453 CTGACATTCACATGATCTTCACTGCTCTATTTATGAGTGTATCTGCTCAACAGATAC 512
Db 309 CTGACATTCACATGATCTTCACTGCTCTATTTATGAGTGTATCTGCTCAACAGATAC 368
QY 513 CTGATCTTTTCAAGTGCAGAAAGAAAGTGAATTTCTACAGAAACCTGCATGCTGCT 572
Db 369 CTGATCTTTTCAAGTGCAGAAAGAAAGTGAATTTCTACAGAAACCTGCATGCTGCT 428
QY 573 GCCAGTCTGGCATGTGGACGCTGGTGTATGTCAATTTGTAGTACCCCTGGTGTCTCCGG 632
Db 429 GCCAGTCTGGCATGTGGACGCTGGTGTATGTCAATTTGTAGTACCCCTGGTGTCTCCGG 488
QY 633 TATGAATTCATGAGAAATACATGAGAGCACTGTTTTAAATTTCACAAGAGCTTGTCT 692
Db 489 TATGAATTCATGAGAAATACATGAGAGCACTGTTTTAAATTTCACAAGAGCTTGTCT 548
QY 693 TACCATATGAGAAATACATGATGATGATGATGATGATGATGATGATGATGATGATG 752
Db 549 TACCATATGAGAAATACATGATGATGATGATGATGATGATGATGATGATGATGATG 608
QY 753 ATTCTGTGTGCTTCCAGGCTCTCATCATTTATGTTAGTGCAGAAAGCTACGCACTCT 812
Db 609 ATTCTGTGTGCTTCCAGGCTCTCATCATTTATGTTAGTGCAGAAAGCTACGCACTCT 668
QY 813 TTACTATCCACAGAGAGTCTGAGGCTCAGCTGAGAAACCTATTTTTTATAGGGGCTATC 872
Db 669 TTACTATCCACAGAGAGTCTGAGGCTCAGCTGAGAAACCTATTTTTTATAGGGGCTATC 728
QY 873 CTGTGTGTGCTTCCCTTACAGTCTTGTAGGATTAATTAATGTTGTGATGATGAT 932
Db 729 CTGTGTGTGCTTCCCTTACAGTCTTGTAGGATTAATTAATGTTGTGATGATGAT 788
QY 933 TCCATATGCTGTAGAGAGAGTGTGATTTATATACGAATCTTCTTGAAGTATACAGCA 992
Db 789 TCCATATGCTGTATACAGAGAGTGTGATTTATATACGAATCTTCTTGAAGTATACAGCA 848
QY 993 ATTAGCTGTATGATTTGCTTCTTGTCTTTTGGGGAGAGCAATGTTTAAAGCAAAAG 1052
Db 849 ATTAGCTGTATGATTTGCTTCTTGTCTTTTGGGGAGAGCAATGTTTAAAGCAAAAG 908
QY 1053 ATATATGGCTATAGGAATTTGTTTGGCGTTAGCCAAACATACAGTATGATATTT 1112
Db 909 ATATATGGCTATAGGAATTTGTTTGGCGTTAGCCAAACATACAGTATGATATTT 968
QY 1113 GCTTCTTTATATTGGGAAT-AAAATGGGATTAAGGGAGATTAAGATGATTTTCAATAC 1171
Db 969 GCTTCTTTATATTGGGAATTAATAATGGGATTAAGGGAGATTAAGATGATTTTCAATAC 1028
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Db 1029 TTGATCAAAACCATGCTTGTATGTATCCAAACCAAAAGAGACTATTAATTAATGCAAGAGCTT 1088
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QY 1232 CATTTAGTCTTATGGGATCCCTCCCATCTCTGAGTATGAGGCTGACAAAGACAGTGT 1291
Db 1089 CATTTAGTCTTATGGGATCCCTCCCATCTCTGAGTATGAGGCTGACAAAGACAGTGT 1148
QY 1292 TGTGATCCACCTGTAGGATTTGCAATATTAATTAATTTTCCAGTACAGATGTGTGTGG 1351
Db 1149 TGTGATCCACCTGTAGGATTTGCAATATTAATTAATTTTCCAGTACAGATGTGTGTGG 1208
QY 1352 CCATGAAAGCAATATGATTTTAAAGATTTTAAAGATTTTAAAGTCTATTTAAGTTC 1411
Db 1209 CCATGAAAGCAATATGATTTTAAAGATTTTAAAGATTTTAAAGTCTATTTAAGTTC 1267
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Db 1388 TCCCTGCTTACCAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATG 1447
QY 1592 GGAAGAAATGATTAATAATTTTCTAGGATGATGATGATGATGATGATGATGATGATG 1651
Db 1448 GGAAGAAATGATTAATAATTTTCTAGGATGATGATGATGATGATGATGATGATGATG 1507
QY 1652 AGA 1654
Db 1508 AGA 1510
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RESULT 4
US-10-975-979-81
; Sequence 81, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Seifert, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Schellin, Kathleen
; APPLICANT: Barnigan, Chris
; APPLICANT: Huff, Valerie
; APPLICANT: Kaytes, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Hiebsch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PHM293
; CURRENT APPLICATION NUMBER: US/10/975,979
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
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; LOCATION: (1) .. (113306)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201) .. (207)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11526) .. (12452)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37954) .. (38097)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98732) .. (98784)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112891) .. (113306)
; US-10-292-798-1007

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Query Match      87.4%; Score 1472.2; DB 17; Length 113306;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 155 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 214
DB 11524 AGGTGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11583
QY 215 AATGACACCCCACTTAATAGAGCTCTAATAGTCTTATTTGGGGGCTGGTGGTGT 274
DB 11584 AATGACACCCCACTTAATAGAGCTCTAATAGTCTTATTTGGGGGCTGGTGGTGT 11643
QY 275 CATTTTCATTTCTTTCTCTGCTGTAATAACACCCGCTGATGACCAATGCGGT 334
DB 11644 CATTTTCATTTCTTTCTCTGCTGTAATAACACCCGCTGATGACCAATGCGGT 11703
QY 335 CATTAACCTGCTGCTGCTGCAAGCTTTTCTGCTGCAAGTCCATTTGCTTGACTTA 394
DB 11704 CATTAACCTGCTGCTGCTGCAAGCTTTTCTGCTGCAAGTCCATTTGCTTGACTTA 11763
QY 395 CCGTACCAAGAAAGACTTGATGTTTGGGCTGCTTCTGCAATTTGTAAGTCCATGCT 454
DB 11764 CCGTACCAAGAAAGACTTGATGTTTGGGCTGCTTCTGCAATTTGTAAGTCCATGCT 11823
QY 455 GGCATCCACATGATCTGACGTTCTTATTTCTATGCTGATCTGCTGCAATGCT 514
DB 11824 GGCATCCACATGATCTGACGTTCTTATTTCTATGCTGATCTGCTGCAATGCT 11883
QY 515 CATTTCTTCAAGTGAAGAAAGCAAGTGAATTTCAAGAAACCTGATGCTGCTGCTG 574
DB 11884 CATTTCTTCAAGTGAAGAAAGCAAGTGAATTTCAAGAAACCTGATGCTGCTGCTG 11943
QY 575 CAGTGTGCAATGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
DB 11944 CAGTGTGCAATGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12003
QY 635 TCGAATCCATGAGGAATTAATAGAGGACCTGTTTAAATTTCAAGAAAGCTTGTCTTA 694
DB 12004 TCGAATCCATGAGGAATTAATAGAGGACCTGTTTAAATTTCAAGAAAGCTTGTCTTA 12063
QY 695 CACATATGGAAGAAATCATCACTATATGATGATCATTTTGTGATGCGGTGCTGAT 754
DB 12064 CACATATGGAAGAAATCATCACTATATGATGATCATTTTGTGATGCGGTGCTGAT 12123
QY 755 TCGTGTGCTTCCAGGCTCTCATCATATGTTGATGAGGAGCAAGCTGACGCTTCT 814
DB 12124 TCGTGTGCTTCCAGGCTCTCATCATATGTTGATGAGGAGCAAGCTGACGCTTCT 12183
QY 815 ACTATCCACACGAGAGTCTGAGCTGAGTGAAGAAACCTATTTTATAGGGTCTCATCT 874
DB 12184 ACTATCCACACGAGAGTCTGAGCTGAGTGAAGAAACCTATTTTATAGGGTCTCATCT 12243
QY 875 TGTGTTGTTCTTCCCTTACAGTCTTTATAGATCTATTAATGTAATGTTGTGACGCTTC 934
DB 12244 TGTGTTGTTCTTCCCTTACAGTCTTTATAGATCTATTAATGTAATGTTGTGACGCTTC 12303

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QY 935 CAATGCTGTAGCAGCAAGTTGATTTTATATAGAAATCTTGAAGTAAAGCAAT 994
DB 12304 CAATGCTGTAGCAGCAAGTTGATTTTATATAGAAATCTTGAAGTAAAGCAAT 12363
QY 995 TAGCTGTATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1054
DB 12364 TAGCTGTATGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 12423
QY 1055 AATTGGCTTAAGGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1114
DB 12424 AATTGGCTTAAGGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 12483
QY 1115 TTCCTTTATATGGAAT-AAAAATGATATAGAGGAGTAAGAAATGATTTCAATCTT 1173
DB 12484 TTCCTTTATATGGAATTAAGAAATGATATAGAGGAGTAAGAAATGATTTCAATCTT 12543
QY 1174 GATCAAAAACCATGCTTGAATGATCAAAAACCAAAAGACATATTAATGCAAGGCCCTCA 1233
DB 12544 GATCAAAAACCATGCTTGAATGATCAAAAACCAAAAGACATATTAATGCAAGGCCCTCA 12603
QY 1234 TTGTATGCTTTATGGAATCCCTCCATCTCTGATGATGAGCCGCTTCAAAAGACATGTTG 1293
DB 12604 TTGTATGCTTTATGGAATCCCTCCATCTCTGATGATGAGCCGCTTCAAAAGACATGTTG 12663
QY 1294 TTGAATCCACCTGAGTGAATATTAATTAATTTTCCAGTACAGAAATGCTGTTGGCC 1353
DB 12664 TTGAATCCACCTGAGTGAATATTAATTAATTTTCCAGTACAGAAATGCTGTTGGCC 12723
QY 1354 CATGAAGCAACATAGTTTAAAGATTTTAAAGATTTTCAATTAAGTCAATTTAGTTCT 1413
DB 12724 CATGAAGCAACATAGTTTAAAGATTTTAAAGATTTTCAATTAAGTCAATTTAGTTCT 12782
QY 1414 CTGTTGAAGCATGCTCTTATGTTTGAATGATCAATCAACCTTTTATGTTCTTCTTCAATC 1473
DB 12783 CTGTTGAAGCATGCTCTTATGTTTGAATGATCAATCAACCTTTTATGTTCTTCTTCAATC 12842
QY 1474 CCACTTCAACATAGGATTAAGTAAATCTGAGCCACCAAGCTCCAAAGACCAAACTCTC 1533
DB 12843 CCACTTCAACATAGGATTAAGTAAATCTGAGCCACCAAGCTCCAAAGACCAAACTCTC 12902
QY 1534 CTTCGCTAACAGGTTAGATGCTCCATTCATCTCATGCTCTGATTAATAAATCTGATTAAGGGG 1593
DB 12903 CTTCGCTAACAGGTTAGATGCTCCATTCATCTCATGCTCTGATTAATAAATCTGATTAAGGGG 12962
QY 1594 AAGAAATAGTTAAATTTTCTAGGATATCACTCTGTAAGAAAGTCACTGCTTGA 1653
DB 12963 AAGAAATAGTTAAATTTTCTAGGATATCACTCTGTAAGAAAGTCACTGCTTGA 13022
QY 1654 A 1654
DB 13023 A 13023

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RESULT 6  
US-10-467-252-52  
Sequence 52, Application US/10467252  
Publication No. US20040115676A1

GENERAL INFORMATION:  
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;  
; APPLICANT: YAO, Monique G.; KALICKI, Deborah A.;  
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandier K.;  
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;  
; APPLICANT: HAFALIA, April J.A.; RAMKUMAR, Jayalaxmi;  
; APPLICANT: JIN, Pei; TANG, Y. Tom;  
; APPLICANT: YUE, Henry; REDDY, Roopa  
; APPLICANT: BURFORD, Neil; LU, Dying Aina M.;  
; APPLICANT: GRAUB, Richard C.; KAHN, Parrah A.;  
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;  
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.  
; APPLICANT: WARREN, Bridget A.; YANG, Junning;  
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee

Db	617	GGCTGCAGAGTCTGGCAGTGTGACGCTGGTGAATTGTCAATGTGGTAACCCGTGTTGTCTC	676
Qy	629	CCGGATATGGAATCCATGAGGAATCAATAGAGAGCACTGTTTAAATTTCACAAAGACT	688
Db	677	CCGGATATGGAATCCATGAGGAATCAATAGAGAGCACTGTTTAAATTTCACAAAGACT	736
Qy	689	TGCTTAACAAATATGTGAAAATCATCAACTATATGATGTCATTTTTGTTCATAGCCGTTC	748
Db	737	TGCTTAACAAATATGTGAAAATCATCAACTATATGATGTCATTTTTGTTCATAGCCGTTC	796
Qy	749	TGATATCTGTGGTCTCCAGGCTCTACATCATATGTGATGGGTGCGAAGCTACGCA	808
Db	797	TGATATCTGTGGTCTCCAGGCTCTACATCATATGTGATGGGTGCGAAGCTACGCA	856
Qy	809	CTCTTTACTATCCACGAGAGTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGT	868
Db	857	CTCTTTACTATCCACGAGAGTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGT	916
Qy	869	CATCCYTGTTGTTTCCCTCCCTACCAAGTCTTATAGATCTATTACTGATGTTGTGAC	928
Db	917	CATCCYTGTTGTTTCCCTCCCTACCAAGTCTTATAGATCTATTACTGATGTTGTGAC	976
Qy	929	GCAATTCGAATGCTGTAGACAGCAAGTTGCATTTATPACGAATCTTCTTGAGGTGAC	988
Db	977	GCAATTCGAATGCTGTAGACAGCAAGTTGCATTTATPACGAATCTTCTTGAGGTGAC	1036
Qy	989	AGCAATTAGCTGTCTATTAATTTGCTTCTCTTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCA	1048
Db	1037	AGCAATTAGCTGTCTATTAATTTGCTTCTCTTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCA	1096

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DB 1097 AAGATATTTGGCTTATGGATTGTGTTTGTGTCGTTAGCCCAAACTACAGATTTCAT 1156

Qy 1109 ATTGCTTCCTTTATATTGGGAAT-AAAATGGGTATAGGGAGGTAAAGAAATGGTATTTC 1167

Db 1157 ATTGCTTCCTTATATGGGATAAAAATGGGTATGGGGAGCTAGAATGTTTCA 1216

1168 TTACTGTCAAAACCATGCTTGATGTACCACAAACAAAGGACTATATAATGCAAGAG 1227

Db 1217 TTACTTGATCAAAACCATGCTTGATGTACCCAAAACAAAAGCATTAATAATGCAGAG 1276

1228 CCTCATTTGTAAGTCCTTATGGGATCCCTCCCATCTCTGAGTGATGGC 1274

[illegible]

12111 CCCCATGTAAGTCCTTAAGGAACTCCCTCCCATCTCTGAGTAGAGGC 1323

## RESULT 7

US-10-017-161-1193  
: Sequence 1193. Application US/10017161

Publication No. US20030143668A1

;; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO

APPLICANT: ASAI, KIYOSHI  
APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI  
TITLE OF INVENTION: NOVEL C PROTEIN-CONTAINING PREPEPTIDES

FILE REFERENCE: 084335/0152

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: CURRENT APPLICATION NUMBER: US/10/017,161
: CURRENT FILING DATE: 2002-12-18

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;; PRIORITY APPLICATION NUMBER: JP 2001/246789  
; PRIORITY FILING DATE: 2001-06-18  
;

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: NUMBER OF SEQ ID NOS: 2430
:
: SOFTWARE: PatentIn Ver. 2.1

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: SEQ ID NO 1193
:
: DIVCNT: 1110

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LENGTH: 1318  
 TYPE: DNA

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; ORGANISM: Homo sapiens
;
; FEATURE:

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; NAME/KEY: source
; LOCATION: (1) - (131A)

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FEATURE: NAME/TYPE: CDS

NAME/KEY: CDS	!
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; LOCATION: (201)...(1118)
US-10-017-161-1193

Query Match      66.4%; Score 1118.8; DB 15; Length 1318;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 155 ATGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGGAATTCCTCTTGCGATCTAT 214
    |||||
DB 185 AGGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGGAATTCCTCTTGCGATCTAT 244

QY 215 AGTGAACCCCACTTAATCAAGCTCTTAATAGTGTATTTAGCGGGCTGGTGGTGT 274
    |||||
DB 245 AGTGAACCCCACTTAATCAAGCTCTTAATAGTGTATTTAGCGGGCTGGTGGTGT 304

QY 275 CATTTCATCTTTCTCTCTGCTGTAAGAAACACCCGGTCACTGACCAATGCGGT 334
    |||||
DB 305 CATTTCATCTTTCTCTCTGCTGTAAGAAACACCCGGTCACTGACCAATGCGGT 364

QY 335 CATTAACTTGGTGGTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTA 394
    |||||
DB 365 CATTAACTTGGTGGTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTA 424

QY 395 CCTCATCAAGAAAGCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTCCATGCT 454
    |||||
DB 425 CCTCATCAAGAAAGCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTCCATGCT 484

QY 455 GCACATCCCAATGTAATCTCACTTCTATATGATGTAATCTGCTGACCAATACCT 514
    |||||
DB 485 GCACATCCCAATGTAATCTCACTTCTATATGATGTAATCTGCTGACCAATACCT 544

QY 515 CATCTTCTTCAAGTGAAGAAAGAAAGTGAATTTCTACAGAAACCTGATCTGTGGCTGC 574
    |||||
DB 545 CATCTTCTTCAAGTGAAGAAAGAAAGTGAATTTCTACAGAAACCTGATCTGTGGCTGC 604

QY 575 CAGTGTCTGGATGTGACGCTGTGTATTTGATTTGTGTAACCCCTGGTGTCTCCGGTA 634
    |||||
DB 605 CAGTGTCTGGATGTGACGCTGTGTATTTGATTTGTGTAACCCCTGGTGTCTCCGGTA 664

QY 635 TGGAAATCCAGAGAAATACAAATGAGAGCACTGTTTAAATTTACAAAGAGCTTGCTTA 694
    |||||
DB 665 TGGAAATCCAGAGAAATACAAATGAGAGCACTGTTTAAATTTACAAAGAGCTTGCTTA 724

QY 695 CACATAATGTAATATCACTAATATATGATGATCTTTTGTGATAGCCGTGCTGAT 754
    |||||
DB 725 CACATAATGTAATATCACTAATATATGATGATCTTTTGTGATAGCCGTGCTGAT 784

QY 755 TCTGTGTGCTTCCAGGTCTTCAATCATTTATGTTGATGTCAGAAAGCTACGCCATCTTT 814
    |||||
DB 785 TCTGTGTGCTTCCAGGTCTTCAATCATTTATGTTGATGTCAGAAAGCTACGCCATCTTT 844

QY 815 ACTATCCCAAGAGAGTTCTGGGCTCAGCTGAAACCTATTTTATATAGGGTCAATCCT 874
    |||||
DB 845 ACTATCCCAAGAGAGTTCTGGGCTCAGCTGAAACCTATTTTATATAGGGTCAATCCT 904

QY 875 TGTGTGTGCTTCCCTACAGTTCTTTAGGATCTATTACTTGAATGTTGACGCAATTC 934
    |||||
DB 905 TGTGTGTGCTTCCCTACAGTTCTTTAGGATCTATTACTTGAATGTTGACGCAATTC 964

QY 935 CAAATGCTGTAGACAGAGTTGATTTTAAAGAAATCTTCTGAGTGTAAACAGCAAT 994
    |||||
DB 965 CAAATGCTGTAGACAGAGTTGATTTTAAAGAAATCTTCTGAGTGTAAACAGCAAT 1024

QY 995 TACCTGTATGATTTGCTTCTCTTTGCTTTGGGGAGAGCAATTTGTTAAGCAAAAGAT 1054
    |||||
DB 1025 TACCTGTATGATTTGCTTCTCTTTGCTTTGGGGAGAGCAATTTGTTAAGCAAAAGAT 1084

QY 1055 AATGAGCTTAATGATTTGTTTGTGTCGTTAGCCCAAACTACAGTATTTCAATTTGC 1114
    |||||
DB 1085 AATGAGCTTAATGATTTGTTTGTGTCGTTAGCCCAAACTACAGTATTTCAATTTGC 1144

QY 1115 TTCCTTATATTTGGGAAT-AAAAATGGGTATAGGGAGGTAAAGATGATTTTCAATTAATT 1173
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DB 1145 TTCCTTATATTTGGGAATAAAAATGGGTATAGGGAGGTAAAGATGATTTTCAATTAATT 1204
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QY 1174 GATCAAAACCAATGCTTGAATGATACCAAAAGAAAGACTATTAATATGCAAGCCCTCA 1233
    |||||
DB 1205 GATCAAAACCAATGCTTGAATGATACCAAAAGAAAGACTATTAATATGCAAGCCCTCA 1264
    |||||

QY 1234 TTGTAGTCTTATAGGATCCCTCCATCTCTGATGATAGGCCGTACAAAGACCA 1287
    |||||
DB 1265 TTGTAGTCTTATAGGATCCCTCCATCTCTGATGATAGGCCGTACAAAGACCA 1318
    |||||

RESULT 8
US-10-467-252-53
; Sequence 53, Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HARFALIA, April J.A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; YANG, Y.Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dying Anna M.;
; APPLICANT: GRAUB, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Derrick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; HARLAND, Lee
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 90012586CB1
; US-10-467-252-53

Query Match      65.7%; Score 1106.2; DB 19; Length 1340;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 513 CTGATCTTCTTCAAGTGAAGCAAGAGATTTCTACAGAAAGTCAGTGTGGCT 572
Db 685 CTGATCTTCTTCAAGTGAAGCAAGAGATTTCTACAGAAAGTCAGTGTGGCT 744
QY 573 GCCAGTGTGGCATGTGAGCGCTGTGATTTGATTTGATGAGTCCCTGGTTGTCTCCG 632
Db 745 GCCAGTGTGGCATGTGAGCGCTGTGATTTGATTTGATGAGTCCCTGGTTGTCTCCG 804
QY 633 TATGGAATCCATGAGGAATTCATATGAGAGCATCTGTTTAAATTTTCACAAAGCTTGGT 692
Db 805 TATGGAATCCATGAGGAATTCATATGAGAGCATCTGTTTAAATTTTCACAAAGCTTGGT 864
QY 693 TACACATGTGAAATTCATCACTATGATAGTATGATTTTGTACAGCCGTGGCTG 752
Db 865 TACACATGTGAAATTCATCACTATGATAGTATGATTTTGTACAGCCGTGGCTG 924
QY 753 ATTCTGTGGTCTTCCAGGTCTTTCATCATTTATGATGAGTGAAGCTACGCCACTCT 812
Db 925 ATTCTGTGGTCTTCCAGGTCTTTCATCATTTATGATGAGTGAAGCTACGCCACTCT 984
QY 813 TTAATATCCCAAGAGATTTGAGGCTCAGCTGAAAGAACTATTTTATAGGGGTGATC 872
Db 985 TTAATATCCCAAGAGATTTGAGGCTCAGCTGAAAGAACTATTTTATAGGGGTGATC 1044
QY 873 CTGTTGTTGTTCTTCCCTACAGTCTTTAGAGTCTATTAATGATGTTGAGAGCAT 932
Db 1045 CTGTTGTTGTTCTTCCCTACAGTCTTTAGAGTCTATTAATGATGTTGAGAGCAT 1104
QY 933 TCCAAATGCTGTAGCAAGAGTGTGATTTATTAACGAAATCTTCTTGAAGTGAACAGA 992
Db 1105 TCCAAATGCTGTAGCAAGAGTGTGATTTATTAACGAAATCTTCTTGAAGTGAACAGA 1164
QY 993 AATAGCTGCTATATTTGCTTCTTGTGTTGGGGGAAAGCATTTGGTTTAAAGCAAAG 1052
Db 1165 AATAGCTGCTATATTTGCTTCTTGTGTTGGGGGAAAGCATTTGGTTTAAAGCAAAG 1224
QY 1053 AATAATGCTTATGAAATTTGTTTGTGCGTTAGCCAAACATCAAGTATCATATTT 1112
Db 1225 AATAATGCTTATGAAATTTGTTTGTGCGTTAGCCAAACATCAAGTATCATATTT 1284
QY 1113 GCTTCCTTATATTTGGGAAT-AAATGGGTATAGGGGAGTAAAGTGTATTCATTAAC 1171
Db 1285 GCTTCCTTATATTTGGGAATAAATGGGTATAGGGGAGTAAAGTGTATTCATTAAC 1344
QY 1172 TTGATCAAAACCATGCTTGAATGTAACCAAAACAAAGACATTAATGCAAGAACCT 1231
Db 1345 TTGATCAAAACCATGCTTGAATGTAACCAAAACAAAGACATTAATGCAAGAACCT 1404
QY 1232 CATTTAGTCTTATGAGGATCCCTCCCATCTGAGTGAATGGC 1274
Db 1405 CATTTAGTCTTATGAGGATCCCTCCCATCTGAGTGAATGGC 1447

RESULT 10
US-10-398-036-22
; Sequence 22, Application US/10398036
; Publication No. US20040137564A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL, Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Jeyalaxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyrung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
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; CURRENT APPLICATION NUMBER: US/10/398,036
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6157025CB1
; US-10-398-036-22
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Query Match 61.2%; Score 1030; DB 19; Length 1499;
Best Local Similarity 98.6%; Pred. No. 1.9e-292;
Matches 1091; Conservative 0; Mismatches 10; Indels 5; Gaps 5;
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QY 157 GTGACTTCCCAAGTATGCTGTGCAACAATACCTCGAAGAAATCTCTTGCAATCTTAATG 216
Db 367 GTGACTTCCCAAGTATGCTGTGCAACAATACCTCGAAGAAATCTCTTGCAATCTTAATG 426
QY 217 TGAACCCCACTTAATACAGCTCTTAATGATGCTTAATGAGGCGGTGGGTGCA 276
Db 427 TGAACCCCACTTAATACAGCTCTTAATGATGCTTAATGAGGCGGTGGGTGCA 486
QY 277 TTTCAATCTTTTCCCTGCTGTAATAATGAACCCGCTCACTGACCAACATGCGGTCA 336
Db 487 TTTCAATCTTTTCCCTGCTGTAATAATGAACCCGCTCACTGACCAACATGCGGTCA 546
QY 337 TTAATCTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTTACC 396
Db 547 TTAATCTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTTACC 606
QY 397 TCATCAAGAGACTTGAATGTTTGGGCTGCCCTTTCGCAAAATTTGAGAGTGCATGCTGC 456
Db 607 TCATCAAGAGACTTGAATGTTTGGGCTGCCCTTTCGCAAAATTTGAGAGTGCATGCTGC 666
QY 457 ACATCCACATGATACCTCAAGTCTTAATGATGATGATGATGATGATGATGATGATGATG 516
Db 667 ACATCCACATGATACCTCAAGTCTTAATGATGATGATGATGATGATGATGATGATGATG 726
QY 517 TCTTCTTCAAGTGAAGCAAGAGTGAATTTTCAAGAAATTCGATGCTGTGGCTGCCA 576
Db 727 TCTTCTTCAAGTGAAGCAAGAGTGAATTTTCAAGAAATTCGATGCTGTGGCTGCCA 786
QY 577 GTCGCTGGCATGTGAGCGCTGTGATTTGATGATGATGATGATGATGATGATGATGATG 636
Db 787 GTCGCTGGCATGTGAGCGCTGTGATTTGATGATGATGATGATGATGATGATGATGATG 846
QY 637 GAATCATGAGGAATATCAATGAGAGCACTGTTTAAATTTTCACAAAGAGCTTGCTTACA 696
Db 847 GAATCATGAGGAATATCAATGAGAGCACTGTTTAAATTTTCACAAAGAGCTTGCTTACA 906
QY 697 CATATGTGAATAATCAATCAATATATATGATGATGATGATGATGATGATGATGATGATG 756
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/ PRIOR FILING DATE: 2001-03-01
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 939
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(939)
US-10-085-233B-3

Query Match      55.8%; Score 939; DB 14; Length 939;
Best Local Similarity 100.0%; Pred. No. 1e-265;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATGCAAAATGTACTTCCCAATATGCTGGCCACAAATCCCTCCGAAATTCCTTTGC 206
DB 1 ATGCAAAATGTACTTCCCAATATGCTGGCCACAAATCCCTCCGAAATTCCTTTGC 60
QY 207 GATCTATATGACACCCCACTTAATCAGGCTCTACTCTAGTGTCTTAATTTGGCGGCTG 266
DB 61 GATCTATATGACACCCCACTTAATCAGGCTCTACTCTAGTGTCTTAATTTGGCGGCTG 120
QY 267 GTGGGTGTCAATTCATTTCTTCTCTGTGTGAAATGAACCCGGTCAAGTACACC 326
DB 121 GTGGGTGTCAATTCATTTCTTCTCTGTGTGAAATGAACCCGGTCAAGTACACC 180
QY 327 ATGGCGGTCAATTAATTTGGTGTGTGTCCACAGGTTTTTCTGTGACAGTGCATTTCCG 386
DB 181 ATGGCGGTCAATTAATTTGGTGTGTGTCCACAGGTTTTTCTGTGACAGTGCATTTCCG 240
QY 387 TTGACCTACTCATCAAGAAGACTTGGATTTGGGCTGCCCTTTCGAAATTTGTGAGT 446
DB 241 TTGACCTACTCATCAAGAAGACTTGGATTTGGGCTGCCCTTTCGAAATTTGTGAGT 300
QY 447 GCCATCTGCACATCCACATGTAAGTCTCAGCTTCTATTTGATGTGATCTGTACCC 506
DB 301 GCCATCTGCACATCCACATGTAAGTCTCAGCTTCTATTTGATGTGATCTGTACCC 360
QY 507 AGATTAATCTATCTTTTCAAGTGAAGCAAGTGTGAATTTCAAGAAATTCGATGCT 566
DB 361 AGATTAATCTATCTTTTCAAGTGAAGCAAGTGTGAATTTCAAGAAATTCGATGCT 420
QY 567 GTGGCTGCAGTCTGGCATGTGAGCGTGTGATTTGTCTATTTGAGTCCCTGTTGTC 626
DB 421 GTGGCTGCAGTCTGGCATGTGAGCGTGTGATTTGTCTATTTGAGTCCCTGTTGTC 480
QY 627 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAAAG 686
DB 481 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAAAG 540
QY 687 CTGGCTTAACATATGTGAAATATCACTATATGATGCTATTTTGTCAAGCCGT 746
DB 541 CTGGCTTAACATATGTGAAATATCACTATATGATGCTATTTTGTCAAGCCGT 600
QY 747 GCTGTATCTGTGTCTTCCAGTCTTCATCATTAATGTGATGAGTGAAGTACAC 806
DB 601 GCTGTATCTGTGTCTTCCAGTCTTCATCATTAATGTGATGAGTGAAGTACAC 660
QY 807 CACTCTTATCTATCCACAGAGGTTCTGGGCTCAGCTGAAAACTTAATTTTATAGG 866
DB 661 CACTCTTATCTATCCACAGAGGTTCTGGGCTCAGCTGAAAACTTAATTTTATAGG 720
QY 867 GTCACTCTTGTGTGTCTTCCCTTACAGTCTTTTATGATCTATTAATTTGAATTTG 926
DB 721 GTCACTCTTGTGTGTCTTCCCTTACAGTCTTTTATGATCTATTAATTTGAATTTG 780
QY 927 AGCATTTCAATGCTGTAGACAGAGTTCATTTTATATAGAAATCTTTGAGTGA 986
DB 781 AGCATTTCAATGCTGTAGACAGAGTTCATTTTATATAGAAATCTTTGAGTGA 840
QY 987 ACAGCAATTAGCTGTATGATTTGCTTCTTTGTCTTTGGGGAAAGCAATGGTTAAG 1046
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DB 841 ACAGCAATTAGCTGTATGATTTGCTTCTTTGTGGGGAAGCATGGTTAAG 900
QY 1047 CAAAGATAATGGCTTATGAAATGTGTTTGTCCCG 1085
DB 901 CAAAGATAATGGCTTATGAAATGTGTTTGTCCCG 939

RESULT 13
US-09-995-225-3
/ Sequence 3, Application US/09995225
/ Publication No. US20020193584A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Chen, Zhi Liang
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Pridle, Cameron
/ TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
/ FILE REFERENCE: AREN-0308
/ CURRENT APPLICATION NUMBER: US/09/995,225
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: PCT/US99/23938
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/253,404
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/255,366
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: 60/270,286
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/282,365
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/270,266
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/282,032
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,358
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,356
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/290,917
/ PRIOR FILING DATE: 2001-05-14
/ PRIOR APPLICATION NUMBER: 60/309,208
/ PRIOR FILING DATE: 2001-07-31
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 918
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-995-225-3

Query Match      54.4%; Score 916.4; DB 9; Length 918;
Best Local Similarity 99.9%; Pred. No. 4.7e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 171 ATGCTGGCCACAATATCTCCAGAAATTCCTTTGGATCTATATGTAACCCCACTTA 230
DB 1 ATGCTGGCCACAATATCTCCAGAAATTCCTTTGGATCTATATGTAACCCCACTTA 60
QY 231 ATCAGCTCTACTTATATGCTTATTTGGCGGGCTGGTGGGTGATTTCCATTTCTTTTC 290
DB 61 ATCAGCTCTACTTATATGCTTATTTGGCGGGCTGGTGGGTGATTTCCATTTCTTTTC 120
QY 291 CTCCTGTGAAATGAACACCCGGTCAAGTGAACCAATGAGCGGTCAATTAATTTGAGT 350
DB 121 CTCCTGTGAAATGAACACCCGGTCAAGTGAACCAATGAGCGGTCAATTAATTTGAGT 180
QY 351 GTCCACAGGTTTTTCTGTGACAGTGCATTTGCTTGAATCTTCACTTCAAGAAACT 410
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Db 181 GTCCACAGCGTTTTCTGTGACGAGTCCATTTGCTTGAACCTACCTCATCAAGAAACT 240  
Qy 411 TGGATGTTGGGCGCCCTCTGCAATTTGTAGTGGCCATGCTGCATCCCATCTAC 470  
Db 241 TGAATGTTGGGCGCCCTCTGCAATTTGTAGTGGCCATGCTGCATCCCATCTAC 300  
Qy 471 CTCACGTTCCATTTCTATGTGTGATCTGTGACAGAGATACCTCATCTTCTCAAGTGC 530  
Db 301 CTCACGTTCCATTTCTATGTGTGATCTGTGACAGAGATACCTCATCTTCTCAAGTGC 360  
Qy 531 AAAAGCAAAAGTGAATTTCAAGAAAATCTGATGCTGTGCTGCAAGTGTGCAATGTC 590  
Db 361 AAAAGCAAAAGTGAATTTCAAGAAAATCTGATGCTGTGCTGCAAGTGTGCAATGTC 420  
Qy 591 ACCGTGATGTTGTCATGTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 650  
Db 421 ACCGTGATGTTGTCATGTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 480  
Qy 651 TACATGAGAGAGCTGTTTAAATTTCAAGAAAGCTGTGCTTACACATATGAAATC 710  
Db 481 TACATGAGAGAGCTGTTTAAATTTCAAGAAAGCTGTGCTTACACATATGAAATC 540  
Qy 711 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 770  
Db 541 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
Qy 771 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 830  
Db 601 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 660  
Qy 831 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCATCCCTGTTGTTCTTCC 890  
Db 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCATCCCTGTTGTTCTTCC 720  
Qy 891 TACAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 950  
Db 721 TACAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
Qy 951 AAGTTGATTTATATGAAATCTTCTGATGTTAAGCAATTTAGCTGCTATGATTTG 1010  
Db 781 AAGTTGATTTATATGAAATCTTCTGATGTTAAGCAATTTAGCTGCTATGATTTG 840  
Qy 1011 CTCTCTGTTGCTTGGGGAGAGCAATGTTTAAAGAAAGATTAATGCTTATGAAAT 1070  
Db 841 CTCTCTGTTGCTTGGGGAGAGCAATGTTTAAAGAAAGATTAATGCTTATGAAAT 900  
Qy 1071 TGTGTTTGTGCGCTTAG 1088  
Db 901 TGTGTTTGTGCGCTTAG 918

RESULT 14  
US-09-995-225-3  
; Sequence 3, Application US/0995225  
; Publication No. US20030139588A9  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi Liang  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Pridie, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G  
; FILE REFERENCE: AREN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253,404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255,366

; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/270,286  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,365  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/270,266  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,032  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,358  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,356  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/290,917  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/309,208  
; PRIOR FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-995-225-3

Query Match 54.4%; Score 916.4; DB 10; Length 918;  
Best Local Similarity 99.9%; Pred. No. 4,7e-259;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 171 ATGCTGGGCAACAATCTCTCAAGAAATCTCTGCGATCTTATAGTGAACCCCACTTA 230  
Db 1 ATGCTGGGCAACAATCTCTCAAGAAATCTCTGCGATCTTATAGTGAACCCCACTTA 60  
Qy 231 ATCAGCTTACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 290  
Db 61 ATCAGCTTACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120  
Qy 291 CTCCTGTAATAATGAACACCGGTCATGATGATGATGATGATGATGATGATGATGATG 350  
Db 121 CTCCTGTAATAATGAACACCGGTCATGATGATGATGATGATGATGATGATGATGATG 180  
Qy 351 GTCCACAGGTTTTCTGTGACAGTGCAATTTGCTTGAACCTCACTCACTCAAGAACT 410  
Db 181 GTCCACAGGTTTTCTGTGACAGTGCAATTTGCTTGAACCTCACTCACTCAAGAACT 240  
Qy 411 TGGATGTTGGGCGCCCTCTGCAATTTGTAGTGGCCATGCTGCATCCCATCTAC 470  
Db 241 TGAATGTTGGGCGCCCTCTGCAATTTGTAGTGGCCATGCTGCATCCCATCTAC 300  
Qy 471 CTCACGTTCCATTTCTATGTGTGATCTGTGACAGAGATACCTCATCTTCTCAAGTGC 530  
Db 301 CTCACGTTCCATTTCTATGTGTGATCTGTGACAGAGATACCTCATCTTCTCAAGTGC 360  
Qy 531 AAAAGCAAAAGTGAATTTCAAGAAAATCTGATGCTGTGCTGCAAGTGTGCAATGTC 590  
Db 361 AAAAGCAAAAGTGAATTTCAAGAAAATCTGATGCTGTGCTGCAAGTGTGCAATGTC 420  
Qy 591 ACCGTGATGTTGTCATGTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 650  
Db 421 ACCGTGATGTTGTCATGTTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 480  
Qy 651 TACATGAGAGAGCTGTTTAAATTTCAAGAAAGCTGTGCTTACACATATGAAATC 710  
Db 481 TACATGAGAGAGCTGTTTAAATTTCAAGAAAGCTGTGCTTACACATATGAAATC 540  
Qy 711 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 770  
Db 541 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
Qy 771 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 830  
Db 601 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 660

QY 831 TTCGAGCTCAGCTGAAAAAAGCTATTTTATAGGGGTCAATCCTGTGTTGTTCTTCCTCC 890  
DB 661 TTCTGGGCTCAGCTGAAAAAGCTATTTTATAGGGGTCAATCCTGTGTTGTTCTTCCTCC 720  
QY 891 TACCAATTTTGAATCTATTTAGTGAATGTTGTAAGCATTCGCAATGCTGTACAGC 950  
DB 721 TACCAATTTTGAATCTATTTAGTGAATGTTGTAAGCATTCGCAATGCTGTACAGC 780  
QY 951 AAGGTTCATTTTATACGAAATCTTCTGAGTGAAGCAATTAAGTGTGATGTTG 1010  
DB 781 AAGGTTCATTTTATACGAAATCTTCTGAGTGAAGCAATTAAGTGTGATGTTG 840  
QY 1011 CTCTCTTTGCTCTTGGGGAGAGCCATGCTTTAAGCAAAAGTAATGGCTTATGGAAT 1070  
DB 841 CTCTCTTTGCTCTTGGGGAGAGCCATGCTTTAAGCAAAAGTAATGGCTTATGGAAT 900  
QY 1071 TGTGTTTGTGCGCTTAG 1088  
DB 901 TGTGTTTGTGCGCTTAG 918

## RESULT 15

US-10-055-106C-1  
; Sequence 1, Application US/10055106C  
; Publication No. US20030017536A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Harland, Lee  
; TITLE OF INVENTION: Novel Polypeptide  
; FILE REFERENCE: P010970AGLK  
; CURRENT APPLICATION NUMBER: US/10/055,106C  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: GB0101739.1  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: US 60/267,341  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-055-106C-1

Query Match 54.4%; Score 916.4; DB 14; Length 918;  
Best Local Similarity 99.9%; Pred. No. 4.7e-259;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 171 ATGCTGGCCACAATACTTCAGAAATTCCTTTCGAGTCTATAGTGAACCCCACTTA 230  
DB 1 ATGCTGGCCACAATACTTCAGAAATTCCTTTCGAGTCTATAGTGAACCCCACTTA 60  
QY 231 ATGAGCTCTACTTCTATAGTCTTATTTGGGGCTGTGGGTGTCATTTCCATTTCTTTT 290  
DB 61 ATGAGCTCTACTTCTATAGTCTTATTTGGGGCTGTGGGTGTCATTTCCATTTCTTTT 120  
QY 291 CTCCTGGTAAATGAACAACCCGTCAGTGAACCAATGAGCGGTCAATTAATTTGATG 350  
DB 121 CTCCTGGTAAATGAACAACCCGTCAGTGAACCAATGAGCGGTCAATTAATTTGATG 180  
QY 351 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTACCTCAATCAAGAACT 410  
DB 181 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTACCTCAATCAAGAACT 240  
QY 411 TGGATTTTGGGCTGCTTTCGCAAAATTTGAGTGCATGTCACATCCCATGTAC 470  
DB 241 TGGATTTTGGGCTGCTTTCGCAAAATTTGAGTGCATGTCACATCCCATGTAC 300  
QY 471 CTCACGTTCTATTTATGATGATCTGTGACACAGATTAATCTTCTTCAAGTGC 530  
DB 301 CTCACGTTCTATTTATGATGATCTGTGACACAGATTAATCTTCTTCAAGTGC 360  
QY 531 AAAGCAAAAGTGAATTTCTACAGAAAATGCATGCTGTGGCTGCCAGTGTGG 590

DB 361 AAAGCAAAAGTGAATTTCTACAGAAAATGCATGCTGTGGCTGCCAGTGTGG 420  
QY 591 AAGCTGAGATTTGATTTGGTACCCGTTGTCCTCCGATAGGAATCAATAGGA 650  
DB 421 AAGCTGAGATTTGATTTGGTACCCGTTGTCCTCCGATAGGAATCAATAGGA 480  
QY 651 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACATATGTGAAAATC 710  
DB 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACATATGTGAAAATC 540  
QY 711 ATCAATATATATATGTCATTTTGTATAGCCGTTGCTGTGATTTCTGTGGTCTTCCAG 770  
DB 541 ATCAATATATATATGTCATTTTGTATAGCCGTTGCTGTGATTTCTGTGGTCTTCCAG 600  
QY 771 GTCCTCATATATGTTGATGGTGAAGAGTGAAGCACTCTTATCTATCCCAAGAG 830  
DB 601 GTCCTCATATATATGTTGATGGTGAAGAGTGAAGCACTCTTATCTATCCCAAGAG 660  
QY 831 TTCGAGCTCAGCTGAAAAAGCTATTTTATAGGGGTCAATCCTGTTGTTTCTTCCTCC 890  
DB 661 TTCTGGGCTCAGCTGAAAAAGCTATTTTATAGGGGTCAATCCTGTTGTTTCTTCCTCC 720  
QY 891 TACCAATTTTGAATCTATTTAGTGAATGTTGTAAGCATTCGCAATGCTGTACAGC 950  
DB 721 TACCAATTTTGAATCTATTTAGTGAATGTTGTAAGCATTCGCAATGCTGTACAGC 780  
QY 951 AAGGTTCATTTTATACGAAATCTTCTGAGTGAAGCAATTAAGTGTGATGTTG 1010  
DB 781 AAGGTTCATTTTATACGAAATCTTCTGAGTGAAGCAATTAAGTGTGATGTTG 840  
QY 1011 CTCTCTTTGCTCTTGGGGAGAGCCATGCTTTAAGCAAAAGTAATGGCTTATGGAAT 1070  
DB 841 CTCTCTTTGCTCTTGGGGAGAGCCATGCTTTAAGCAAAAGTAATGGCTTATGGAAT 900  
QY 1071 TGTGTTTGTGCGCTTAG 1088  
DB 901 TGTGTTTGTGCGCTTAG 918

Search completed: September 10, 2005, 03:39:13  
Job time : 1218.69 secs



PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
disorders.

PS Claim 15; Page 101; 105pp; English.

XX The invention relates to an isolated polypeptide, which is a G-protein  
XX coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
XX receptor type proteins (GPCRs), designated the 93870 receptor. The  
CC polypeptides, nucleic acid molecules and antibodies of the invention are  
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
CC monitoring clinical trials or pharmacogenetics), or in methods of  
CC treatment (e.g. therapeutic and prophylactic). They are useful in  
CC creating and diagnosing conditions related to aberrant activity or  
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
CC disorders, or bone marrow mononuclear disorders, as well as cellular  
CC proliferative and/or differentiative disorders, hormonal disorders,  
CC neurological disorders, cardiovascular disorders, viral diseases, liver  
CC disorders, and pain and metabolic disorders. Conditions that can be  
CC treated include cancer, diabetes mellitus, hypothyroidism,  
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or  
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,  
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,  
CC Huntington's disease, heart failure, angina pectoris, myocardial  
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
CC transgenic animals are useful for studying the function and/or activity  
CC of a 93870 protein and for identifying and/or evaluating modulators of  
CC 93870 activities. The polynucleotides of the invention can be used in  
CC gene therapy. This sequence represents the human G-protein coupled  
XX receptor type protein of the invention

XX Sequence 313 AA;

Query Match 100.0%; Score 1637; DB 5; Length 313;

Best Local Similarity 100.0%; Pred. No. 9.5e-175; Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMGHNTSRNSGCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60  
DB 1 MOKCDPSPMGHNTSRNSGCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60  
QY MAVINLVVHVSFVLLVTPFRLLTYLIKTTWFGSLPCKFVSAMHIMHMLTFLFYVILVT 120  
DB 61 MAVINLVVHVSFVLLVTPFRLLTYLIKTTWFGSLPCKFVSAMHIMHMLTFLFYVILVT 120  
QY 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIIVPLVVSRYGHEEYNEBHCFFKHE 180  
DB 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIIVPLVVSRYGHEEYNEBHCFFKHE 180  
QY 181 LATYVKIINMYVIVIAVAVALVLPQVFIIMAMQKRLSHLSHQEFMAQDKNLPFFIG 240  
DB 181 LATYVKIINMYVIVIAVAVALVLPQVFIIMAMQKRLSHLSHQEFMAQDKNLPFFIG 240  
QY 241 VILVCFPLQPFRIYLVVWTSNACSRYAFYNEIFLSTVTAISCYDILLFPVGGSHWPK 300  
DB 241 VILVCFPLQPFRIYLVVWTSNACSRYAFYNEIFLSTVTAISCYDILLFPVGGSHWPK 300  
QY 301 OKIIGLMNCVLCR 313  
DB 301 OKIIGLMNCVLCR 313  
RESULT 2  
ID AAB71325 standard; protein; 313 AA.  
XX AAB71325;  
XX 19-NOV-2002 (first entry)  
XX

DE Human GCRBC-4 INCYTE ID 90012430CD1 SEQ ID 4.

XX GCRBC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
XX neuroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
XX prozoocide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
XX Parkinson's disease; Crohn's disease; constipation; infection; receptor;  
XX gene therapy.

OS Homo sapiens.

PN WO200263004-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002MO-US003635.

XX 07-FEB-2001; 2001US-0267322P.

PR 23-FEB-2001; 2001US-0271215P.

PR 08-MAR-2001; 2001US-0274551P.

PR 23-MAR-2001; 2001US-0278507P.

PR 30-MAR-2001; 2001US-0280597P.

PR 02-APR-2001; 2001US-0281107P.

PR 06-APR-2001; 2001US-0282121P.

XX (INCYTE) INCYTE GENOMICS INC.

PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;

PI Kallik DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AUA;

PI Ramkumar Y, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;

PI Grail RC, Khan FA, Walsh RT, Leon CH, Richardson TW, Griffin JA;

PI Warren BA, Yang J, Lee EA, Harland L;

XX WPI; 2002-627557/67.

DR N-PSDB; AAF8583.

PT New human G-protein coupled receptors (GCRBC), useful for diagnosing or

PT treating a disease or condition associated with decreased expression or

PT over expression of functional GCRBCs e.g. cancer, Alzheimer's and

PT Parkinson's.

XX Claim 65; Page 164-165; 239pp; English.

XX This invention describes novel polypeptides which have anti-HIV,

XX antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,

XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,

XX antibacterial, fungicide and prozoocidal activity. The products of the

XX invention are useful for treating a disease or condition associated with

XX decreased expression or over expression of functional G-protein coupled

XX receptors (GCRBC), while antibodies generated against the polypeptide of

XX the invention are useful for diagnosing a condition or disease associated

XX with the expression of GCRBC e.g. arteriosclerosis, cirrhosis, cancer,

XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,

XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.

XX The compounds described in the invention can be used for gene therapy.

XX AAB71322-AAB71369 represent the GCRBC proteins encoded by AAF8580-

XX AAF8627 described in the disclosure of the invention

XX Sequence 313 AA;

Query Match 99.8%; Score 1634; DB 5; Length 313;

Best Local Similarity 99.7%; Pred. No. 2.1e-174; Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMGHNTSRNSGCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60  
DB 1 MOKCDPSPMGHNTSRNSGCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60  
QY 61 MAVINLVVHVSFVLLVTPFRLLTYLIKTTWFGSLPCKFVSAMHIMHMLTFLFYVILVT 120  
DB 61 MAVINLVVHVSFVLLVTPFRLLTYLIKTTWFGSLPCKFVSAMHIMHMLTFLFYVILVT 120  
QY 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIIVPLVVSRYGHEEYNEBHCFFKHE 180  
DB 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIIVPLVVSRYGHEEYNEBHCFFKHE 180

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Db      121 RYLFKCKDKVEFRRLAHVAASAGMTLVTVLVPLVVSRYGHEHNEHCFFKHKE 180
Qy      181 LAYTYVYKINMYIPIFIYIAVAVILLVQVFIIMAMOKLRHSLSHOEFMAQLKNLFFIG 240
Db      181 LAYTYVYKINMYIPIFIYIAVAVILLVQVFIIMAMOKLRHSLSHOEFMAQLKNLFFIG 240
Qy      241 VILVCFPLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSHMPK 300
Db      241 VILVCFPLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSHMPK 300
Qy      301 QKIIGLWNCVLCR 313
Db      301 QKIIGLWNCVLCR 313

RESULT 3
AAG80969
ID      AAG80969 standard; protein; 312 AA.
XX
AC      AAG80969;
XX
DT      28-AUG-2001 (first entry)
XX
DE      Human nGRCR16 #2.
XX
KW      G, protein-coupled receptor; nGRCR; seven transmembrane receptor;
KW      signal transduction; schizophrenia; thyroid disorder; renal failure;
KW      rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW      cardiovascular disease; proliferative disorder; hormonal disorder;
KW      neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW      attention deficit-hyperactivity disorder; attention deficit disorder;
KW      Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW      rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW      neuroprotective.
XX
OS      Homo sapiens.
XX
PN      MO200136473-A2.
XX
PD      25-MAY-2001.
XX
PF      16-NOV-2000; 2000WO-US031581.
XX
PR      16-NOV-1999; 99US-0165838P.
PR      17-NOV-1999; 99US-0166071P.
PR      19-NOV-1999; 99US-0166678P.
PR      28-DEC-1999; 99US-0173396P.
PR      22-FEB-2000; 2000US-0184129P.
PR      28-FEB-2000; 2000US-0185421P.
PR      28-FEB-2000; 2000US-0185549P.
PR      02-MAR-2000; 2000US-0186530P.
PR      03-MAR-2000; 2000US-0186811P.
PR      09-MAR-2000; 2000US-0188114P.
PR      17-MAR-2000; 2000US-0190310P.
PR      21-MAR-2000; 2000US-0190800P.
PR      20-APR-2000; 2000US-0198588P.
PR      02-MAY-2000; 2000US-0201190P.
PR      08-MAY-2000; 2000US-0203111P.
PR      25-MAY-2000; 2000US-0207094P.
XX
PA      (PHMA ) PHARMACIA & UPJOHN CO.
XX
PI      Vogel I, G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J,
XX      Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX      WPI; 2001-369826/41.
XX      N-PSDB; AAS1009.
XX      New G protein-coupled receptor (nGRCR-x) and its encoding polynucleotide
XX      useful for diagnosing and treating e.g. schizophrenia.
XX      Claim 37; Page 90; 261pp; English.

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XX      The present invention relates to novel G protein-coupled receptors
CC      (nGRCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC      31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC      one such G protein-coupled receptor. GPCRs are also known as seven
CC      transmembrane receptors and function in signal transduction. The nGRCR
CC      coding sequences are useful for screening a human to diagnose a disorder
CC      affecting the brain or a genetic predisposition, specifically
CC      schizophrenia. nGRCR are useful for identifying compounds useful for
CC      treating schizophrenia. Detection of nGRCR in a sample is useful as a
CC      diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC      failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC      metabolic and cardiovascular diseases, proliferative disorders and
CC      hormonal disorders. Modulators of nGRCR activity have the utility for
CC      treating neurological disorders, including schizophrenia, ADHD/ADD
CC      (attention deficit-hyperactivity disorder/attention deficit disorder),
CC      and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC      migraine and senile dementia. Additional disorders include inflammatory
CC      conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC      disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC      diseases e.g. inflammatory bowel disease
XX
SQ      Sequence 312 AA:
XX
Query Match      98.4%; Score 1610; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 1e-171;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      5 DPFSGMGNHSTRSSCDPIVTPHLISLFLVIGLVGVISILFLVKNMTRSVTTMAVI 64
Db      4 DPFSGMGNHSTRSSCDPIVTPHLISLFLVIGLVGVISILFLVKNMTRSVTTMAVI 63
Qy      65 NLVVHVSFLLTVPPFLTYLIKTTMFGLPCKFVSAMLIHMYLTFLLPVVILVTRYLI 124
Db      64 NLVVHVSFLLTVPPFLTYLIKTTMFGLPCKFVSAMLIHMYLTFLLPVVILVTRYLI 123
Qy      125 FFKCKDKVEFRRLAHVAASAGMTLVTVLVPLVVSRYGHEHNEHCFFKHKLAYT 184
Db      124 FFKCKDKVEFRRLAHVAASAGMTLVTVLVPLVVSRYGHEHNEHCFFKHKLAYT 183
Qy      185 YVKIINMYIPIFIYIAVAVILLVQVFIIMAMOKLRHSLSHOEFMAQLKNLFFIGIYLV 244
Db      184 YVKIINMYIPIFIYIAVAVILLVQVFIIMAMOKLRHSLSHOEFMAQLKNLFFIGIYLV 243
Qy      245 CFLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSHMPKQKI 304
Db      244 CFLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSHMPKQKI 303
Qy      305 GLMNCVLCR 313
Db      304 GLMNCVLCR 312

RESULT 4
ABG93787
ID      ABG93787 standard; protein; 312 AA.
XX
AC      ABG93787;
XX
DT      26-NOV-2002 (first entry)
XX
DE      Human G protein-coupled receptor protein, nGRCR-16.
XX
KW      Human; receptor; G protein-coupled receptor; GPCR; nGRCR; beGRCR;
KW      nG protein coupled receptor; communication; serpentine structure;
KW      seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW      genetic predisposition; brain; immune response; gene therapy;
KW      anxiety disorder; depression; bipolar disorder; schizophrenia;
KW      Huntington's disease; dyskinesia; manic depression; stroke;
KW      Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW      tranquiliser.
XX
OS      Homo sapiens.

```





Query Match 98.4%; Score 1610; DB 5; Length 367;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-171;  
 Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DFPSPMGHNTSRNSCDPIVTPHLISLFTVLIGLVGVISILFLVKNMTRSVTTMAVI 64  
 |||||  
 DB 59 DFPSPMGHNTSRNSCDPIVTPHLISLFTVLIGLVGVISILFLVKNMTRSVTTMAVI 118  
 |||||

QY 65 NLVVHVSFLTPFRLTYLIKTTMFGLPCKFVSAMLIHMYLTFELFYVVLVTRYL 124  
 |||||  
 DB 119 NLVVHVSFLTPFRLTYLIKTTMFGLPCKFVSAMLIHMYLTFELFYVVLVTRYL 178  
 |||||

QY 125 FPKCKDKEFRYRLAHVAASAGMTLVIVVPLVSRVGIHEEYNEHCFFKHKLAYT 184  
 |||||  
 DB 179 FPKCKDKEFRYRLAHVAASAGMTLVIVVPLVSRVGIHEEYNEHCFFKHKLAYT 238  
 |||||

QY 185 YVKIINMYIVFVIAVAVILLVFOVFIIMLVOKLRSLSHOEFMAQLKNLFFIGVILV 244  
 |||||  
 DB 239 YVKIINMYIVFVIAVAVILLVFOVFIIMLVOKLRSLSHOEFMAQLKNLFFIGVILV 298  
 |||||

QY 245 CFLPYQFPRITYLVNVTSHNACSKVAFYNEIFLSTVAISCYDLLFVFGSHWFKXII 304  
 |||||  
 DB 299 CFLPYQFPRITYLVNVTSHNACSKVAFYNEIFLSTVAISCYDLLFVFGSHWFKXII 358  
 |||||

QY 305 GLMNCVLCR 313  
 |||||  
 DB 359 GLMNCVLCR 367  
 |||||

RESULT 6  
 ADC86555  
 ID ADC86555 standard; protein; 448 AA.

AC ADC86555;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human GPCR protein SEQ ID NO:1008.  
 XX  
 DE Human GPCR; guanosine triphosphate-binding protein coupled receptor;  
 XX  
 KM gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX BE1270724-A2.  
 XX  
 PD 02-JAN-2003.  
 XX  
 PF 18-JUN-2002; 2002EP-00013517.  
 XX  
 PR 18-JUN-2001; 2001JP-00246789.  
 XX  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 XX  
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;  
 XX  
 DR N-PSDB; ADC86554.  
 XX  
 PT New polynucleotide, useful for preparing a composition for treating a  
 PT patient in need of increased or suppressed activity or expression of the  
 PT guanosine triphosphate-binding protein coupled receptor.  
 XX  
 PS Claim 2; SEQ ID NO 1008; 28pp; English.  
 XX  
 CC The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The protein

CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.  
 XX  
 SQ Sequence 448 AA;  
 SQ

Query Match 98.4%; Score 1610; DB 7; Length 448;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-171;  
 Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DFPSPMGHNTSRNSCDPIVTPHLISLFTVLIGLVGVISILFLVKNMTRSVTTMAVI 64  
 |||||  
 DB 4 DFPSPMGHNTSRNSCDPIVTPHLISLFTVLIGLVGVISILFLVKNMTRSVTTMAVI 63  
 |||||

QY 65 NLVVHVSFLTPFRLTYLIKTTMFGLPCKFVSAMLIHMYLTFELFYVVLVTRYL 124  
 |||||  
 DB 64 NLVVHVSFLTPFRLTYLIKTTMFGLPCKFVSAMLIHMYLTFELFYVVLVTRYL 123  
 |||||

QY 125 FPKCKDKEFRYRLAHVAASAGMTLVIVVPLVSRVGIHEEYNEHCFFKHKLAYT 184  
 |||||  
 DB 124 FPKCKDKEFRYRLAHVAASAGMTLVIVVPLVSRVGIHEEYNEHCFFKHKLAYT 183  
 |||||

QY 185 YVKIINMYIVFVIAVAVILLVFOVFIIMLVOKLRSLSHOEFMAQLKNLFFIGVILV 244  
 |||||  
 DB 184 YVKIINMYIVFVIAVAVILLVFOVFIIMLVOKLRSLSHOEFMAQLKNLFFIGVILV 243  
 |||||

QY 245 CFLPYQFPRITYLVNVTSHNACSKVAFYNEIFLSTVAISCYDLLFVFGSHWFKXII 304  
 |||||  
 DB 244 CFLPYQFPRITYLVNVTSHNACSKVAFYNEIFLSTVAISCYDLLFVFGSHWFKXII 303  
 |||||

QY 305 GLMNCVLCR 313  
 |||||  
 DB 304 GLMNCVLCR 312  
 |||||

RESULT 7  
 AAM48989  
 ID AAM48989 standard; protein; 305 AA.

AC AAM48989;  
 XX  
 DT 03-MAY-2002 (first entry)  
 XX  
 DE Human testis originated G-protein coupled receptor TGR10.  
 XX  
 DE Human testis originated G-protein coupled receptor; TGR10; inflammatory;  
 XX  
 KM cytosolic; immunomodulator; cardiant; neuroprotective; gene therapy;  
 KM inflammation; nervous system disease; circulatory system disease; cancer;  
 KM metabolic disease; immunological disease; gastrointestinal disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200196567-A1.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 14-JUN-2001; 2001WO-JP005061.  
 XX  
 PR 15-JUN-2000; 2000JP-00184596.  
 XX  
 PR 19-JUL-2000; 2000JP-00223887.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 XX  
 DR N-PSDB; AAL44713.  
 XX  
 PT Human testis-originated G protein-coupled receptor protein TGR10 and  
 PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.  
 PT diseases of central nervous system, inflammations and diseases of  
 PT circulatory system.  
 XX  
 PS Claim 1; Fig 2; 110pp; Japanese.

CC The present invention provides the protein and coding sequences of a  
CC novel human testis-originated G protein-coupled receptor protein TGR10.  
CC The sequences can be used in the development of drugs for the treatment  
CC of diseases of the central nervous system, inflammations, diseases of the  
CC circulatory system, cancer, metabolic diseases, immunological diseases,  
CC and diseases of the gastrointestinal system. The present sequence is the  
CC protein of the invention  
XX

SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 5; Length 305;  
Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MEGHNTSRNSCDPIVTPHLLISLYPIVLIGGLVGVISILFLVKNKTSVTTMAVINLVV 68  
DB 1 MEGHNTSRNSCDPIVTPHLLISLYPIVLIGGLVGVISILFLVKNKTSVTTMAVINLVV 60  
QY 69 VHSVFLTVFPRLTYLIKKTWFGLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128  
DB 61 VHSVFLTVFPRLTYLIKKTWFGLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120  
QY 129 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGHIEBNEEHCFFKHKLATYYVKI 188  
DB 121 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGHIEBNEEHCFFKHKLATYYVKI 180  
QY 189 INYMIYFIYIAVAVLLVFOVFIIMLMVOKLRHSLSHOEFPMAOLKNLFFIGVILVCFPL 248  
DB 181 INYMIYFIYIAVAVLLVFOVFIIMLMVOKLRHSLSHOEFPMAOLKNLFFIGVILVCFPL 240  
QY 249 YQFFRIYILNVVTHSNACSKVAFYNEIFLSVTAISCYDLLFVFGSGHMFQKIIIGLMN 308  
DB 241 YQFFRIYILNVVTHSNACSKVAFYNEIFLSVTAISCYDLLFVFGSGHMFQKIIIGLMN 300  
QY 309 CYLCR 313  
DB 301 CYLCR 305

RESULT 8  
AAB71326  
ID AAB71326 standard; protein; 305 AA.

AC AAB71326;

DT 19-NOV-2002 (first entry)

DE Human GCREC-5 INCYTE ID 90012586CD1 SEQ ID 5.

KW GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
KW cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
KW cerebroprotective; antiinflammatory; vinicide; antibacterial; fungicide;  
KW protozoocide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection; receptor;  
KW gene therapy.

OS Homo sapiens.

PN WO200263004-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002WO-US003635.

XX 07-FEB-2001; 2001US-0267322P.

XX 23-FEB-2001; 2001US-0271215P.

XX 08-MAR-2001; 2001US-0274551P.

XX 23-MAR-2001; 2001US-0278507P.

XX 30-MAR-2001; 2001US-0280597P.

XX 02-APR-2001; 2001US-0281107P.

XX 06-APR-2001; 2001US-0282121P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
PI Kallick DA, Gandhi AR, Walla NK, Arvzu C, Elliott VS, Hafalia AUA;  
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee EA, Harland L;  
XX WPI; 2002-627557/67.

DR N-PSDB; AAF88584.

PT New human G-protein coupled receptors (GCREC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and  
PT Parkinson's.

PS Claim 66; Page 165-166; 239pp; English.

CC This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, vinicide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GCREC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAB71322-AAB71369 represent the GCREC proteins encoded by AAF88580-  
CC AAF88627 described in the disclosure of the invention

SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 5; Length 305;  
Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MEGHNTSRNSCDPIVTPHLLISLYPIVLIGGLVGVISILFLVKNKTSVTTMAVINLVV 68  
DB 1 MEGHNTSRNSCDPIVTPHLLISLYPIVLIGGLVGVISILFLVKNKTSVTTMAVINLVV 60  
QY 69 VHSVFLTVFPRLTYLIKKTWFGLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128  
DB 61 VHSVFLTVFPRLTYLIKKTWFGLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120  
QY 129 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGHIEBNEEHCFFKHKLATYYVKI 188  
DB 121 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGHIEBNEEHCFFKHKLATYYVKI 180  
QY 189 INYMIYFIYIAVAVLLVFOVFIIMLMVOKLRHSLSHOEFPMAOLKNLFFIGVILVCFPL 248  
DB 181 INYMIYFIYIAVAVLLVFOVFIIMLMVOKLRHSLSHOEFPMAOLKNLFFIGVILVCFPL 240  
QY 249 YQFFRIYILNVVTHSNACSKVAFYNEIFLSVTAISCYDLLFVFGSGHMFQKIIIGLMN 308  
DB 241 YQFFRIYILNVVTHSNACSKVAFYNEIFLSVTAISCYDLLFVFGSGHMFQKIIIGLMN 300  
QY 309 CYLCR 313  
DB 301 CYLCR 305

RESULT 9  
AAG79446  
ID AAG79446 standard; protein; 305 AA.

AC AAG79446;

DT 15-NOV-2002 (first entry)

XX PFI-021.

XX DE

KM Human; G-protein coupled receptor; GPCR; PFI-021;  
 KM peripheral blood mononuclear cell; BMC; breast; inflammation; allergy;  
 KM respiratory; neurology; psychology; urogenital disease;  
 KM reproductive dysfunction; sexual dysfunction; cancer; tissue repair;  
 KM dermatology; skin pigmentation; photocaging; frailty; osteoporosis;  
 KM metabolic disease; cardiovascular disease; sleep disorder; hair loss;  
 KM gastrointestinal disease; anti-infection; sensory organ disorder.  
 OS Homo sapiens.  
 XX EPI225183-A2.  
 PN EPI225183-A2.  
 XX 24-JUL-2002.  
 PD 09-JAN-2002; 2002EP-00250128.  
 XX 23-JAN-2001; 2001GB-00001739.  
 PR (PFI2 ) PFIZER LTD.  
 PA (PFI2 ) PFIZER INC.  
 XX Harland L;  
 PI WPI; 2002-601226/65.  
 DR N-PSDB; ABA00160.  
 XX New human G-protein coupled receptor involved in signal transduction,  
 PT useful to treat disorders associated with its expression or activity such  
 as inflammation, allergy and cancer.  
 XX Claim 16; Fig 2; 8pp; English.  
 PS This sequence represents a human G-protein coupled receptor (GPCR), PFI-  
 CC 021. Expressed sequence tags of the PFI-021 sequence are mainly found in  
 CC cDNA libraries from peripheral blood mononuclear cells. Two ESTs have  
 CC been identified in libraries derived from breast mRNA. PFI-021 and the  
 CC corresponding cDNA are used to treat a patient needing altered activation  
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,  
 CC neurology, psychology, urogenital disease, reproductive and sexual  
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin  
 CC pigmentation disorders, photocaging, frailty, osteoporosis, metabolic  
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-  
 CC infection, sensory organ disorders, sleep disorders and hair loss  
 XX Sequence 305 AA;  
 SQ

Query Match 96.9%; Score 1587; DB 5; Length 305;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLSLSTYFVLIGLVGVISILFLVKNKTSVTTMAVINLV 68  
 DB 1 MGHNTSRNSCDPIVTPHLSLSTYFVLIGLVGVISILFLVKNKTSVTTMAVINLV 60  
 QY 69 VHSVFLTVPPRLTYLIKKTMMFGLPCKFVSAMLIHMYLFLFYVILVTRYLIFPKC 128  
 DB 61 VHSVFLTVPPRLTYLIKKTMMFGLPCKFVSAMLIHMYLFLFYVILVTRYLIFPKC 120  
 QY 129 KDKVEFYRKLAAVAASAGMWTLYIVVPLVVSRYGHEEYNEBEHCFKHKLATYYVKI 188  
 DB 121 KDKVEFYRKLAAVAASAGMWTLYIVVPLVVSRYGHEEYNEBEHCFKHKLATYYVKI 180  
 QY 189 INMYVIFIAVAIVLVFQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFPL 248  
 DB 181 INMYVIFIAVAIVLVFQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFPL 240  
 QY 249 YQFPRILYANVWTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSGHMPKOKIIGLMN 308  
 DB 241 YQFPRILYANVWTHSNAGSKVAFYNEIFLSTATISCYDLLFVFGSGHMPKOKIIGLMN 300  
 QY 309 CVLCR 313  
 DB 301 CVLCR 305

RESULT 10  
 AB04069  
 ID AB04069 standard; protein; 305 AA.  
 AC AB04069;  
 XX 11-OCT-2002 (first entry)  
 DT Human G protein coupled receptor hrUP29.  
 DE Human G protein coupled receptor hrUP29.  
 XX Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;  
 KM hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200242461-A2.  
 XX 30-MAY-2002.  
 PD 26-NOV-2001; 2001WO-US044386.  
 XX 27-NOV-2000; 2000US-0253404P.  
 PR 12-DEC-2000; 2000US-0253466P.  
 PR 20-FEB-2001; 2001US-0270266P.  
 PR 20-FEB-2001; 2001US-0270286P.  
 PR 06-APR-2001; 2001US-0282032P.  
 PR 06-APR-2001; 2001US-0282356P.  
 PR 06-APR-2001; 2001US-0282358P.  
 PR 06-APR-2001; 2001US-0282365P.  
 PR 14-MAY-2001; 2001US-0290917P.  
 PR 31-JUL-2001; 2001US-0309208P.  
 XX (AREN-) ARENA PHARM INC.  
 PA Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;  
 PI WPI; 2002-566565/60.  
 DR N-PSDB; ABR04867.  
 XX Novel endogenous and non-endogenous versions of G protein-coupled  
 PT receptor useful for identification of candidate compounds as receptor  
 agonists or antagonists for use as therapeutic agents.  
 XX Claim 5; Page 57-58; 84pp; English.  
 PS The present invention provides the protein and coding sequences of  
 CC several human G-protein coupled receptors (GPCRs). These can be used in  
 CC the identification of candidate compounds as receptor agonists or inverse  
 CC agonists having applicability as therapeutic agents. The present sequence  
 CC is a GPCR protein of the invention  
 XX Sequence 305 AA;  
 SQ

Query Match 96.9%; Score 1587; DB 5; Length 305;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLSLSTYFVLIGLVGVISILFLVKNKTSVTTMAVINLV 68  
 DB 1 MGHNTSRNSCDPIVTPHLSLSTYFVLIGLVGVISILFLVKNKTSVTTMAVINLV 60  
 QY 69 VHSVFLTVPPRLTYLIKKTMMFGLPCKFVSAMLIHMYLFLFYVILVTRYLIFPKC 128  
 DB 61 VHSVFLTVPPRLTYLIKKTMMFGLPCKFVSAMLIHMYLFLFYVILVTRYLIFPKC 120  
 QY 129 KDKVEFYRKLAAVAASAGMWTLYIVVPLVVSRYGHEEYNEBEHCFKHKLATYYVKI 188  
 DB 121 KDKVEFYRKLAAVAASAGMWTLYIVVPLVVSRYGHEEYNEBEHCFKHKLATYYVKI 180  
 QY 189 INMYVIFIAVAIVLVFQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFPL 248  
 DB 181 INMYVIFIAVAIVLVFQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFPL 240

DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 240  
QY 249 YQFFRIYLVNVTTHSNACSSKVAFYNEIFLSTAIISCVDLLLFFVGSGHWFQKIIIGLWN 308  
DB 241 YQFFRIYLVNVTTHSNACNSKVAFYNEIFLSTAIISCVDLLLFFVGSGHWFQKIIIGLWN 300  
QY 309 CVLCCR 313  
DB 301 CVLCCR 305  
RESULT 11  
AAU99179  
ID AAU99179 standard; protein; 305 AA.  
XX AAU99179;  
AC 24-SEP-2002 (first entry)  
XX  
DE Human G protein-coupled receptor IGS70.  
XX  
XX Human; G protein-coupled receptor; GPCR; IGS70; CNS;  
KW psychiatric disorder; central nervous system disorder; schizophrenia;  
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;  
KW heart failure; angina pectoris; myocardial infarction; kidney disease;  
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;  
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;  
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;  
KW osteoporosis; allergy.  
XX  
OS Homo sapiens.  
XX  
PN MO200244212-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 23-NOV-2001; 2001MO-EP013706.  
XX  
PR 30-NOV-2000; 2000EP-00204280.  
PR 05-DEC-2000; 2000US-0251045P.  
XX  
PA (SOLV ) SOLVAY PHARM BV.  
PI Deleernijder W, Blockx H, De Moor L;  
DR WPI: 2002-527703/56.  
DR N-PSDB; ABK97351.  
XX  
PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating  
PT dysfunctions, disorders or disease related to lung, bone marrow, spinal  
PT cord immune system.  
XX  
PS Claim 25; Page 7; 58bp; English.  
XX  
XX The invention relates to a G protein-coupled receptor (GPCR) IGS70  
CC polypeptide including sequences that are 98-99.6% identical. Also  
CC included are the polynucleotide encoding IGS70 (including sequences 98-  
CC 99.6% identical to the polynucleotide or the DNA insert contained in  
CC plasmid CBS 109818), a hybridization probe derived from the  
CC polynucleotide, a DNA or RNA expression system producing IGS70, a host  
CC comprising the expression system, IGS70 receptor membrane preparation  
CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is  
CC useful for diagnosing a disease or a susceptibility to disease in a  
CC subject related to expression or activity of the IGS70 polypeptide in a  
CC subject by determining the presence or absence of mutation in the  
CC nucleotide sequence encoding IGS70 in the genome of the subject in a  
CC sample derived from the subject. IGS70 is also useful identifying agonist  
CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified  
CC ant/agonists are useful for treating psychiatric and central nervous  
CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,  
CC multiple sclerosis, anxiety, cardiovascular diseases such as heart  
CC failure, angina pectoris, myocardial infarction, kidney disease such as  
CC renal failure, gastrointestinal disorders such as irritable bowel

CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,  
CC inflammation, cancers, asthma, infection (such as bacterial, viral,  
CC fungal, protozoal) especially human immunodeficiency virus infection  
CC (HIV), diabetes, osteoporosis and allergies. The present sequence  
CC represents the human GPCR IGS70  
XX  
SQ Sequence 305 AA;  
Query Match 96.9%; Score 1587; DB 5; Length 305;  
Best Local Similarity 99.7%; Pred. No. 3,8e-163;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MEGHNTSRNNSCDPIVTPHLISLPIVILIGLVGISILFLVKNKNTSVTTMAVINLV 68  
DB 1 MEGHNTSRNNSCDPIVTPHLISLPIVILIGLVGISILFLVKNKNTSVTTMAVINLV 60  
QY 69 VHSVFLTVPPRLTYLTKTMMFGCLPCKFVSAMHIMYLTFLFYVILVTRYLIFPKC 128  
DB 61 VHSVFLTVPPRLTYLTKTMMFGCLPCKFVSAMHIMYLTFLFYVILVTRYLIFPKC 120  
QY 129 KDKVEFRKLAHVAASAGMTLVIVIVPLVVSRYGHEEVNEBCHCFKHELAATYVYKI 188  
DB 121 KDKVEFRKLAHVAASAGMTLVIVIVPLVVSRYGHEEVNEBCHCFKHELAATYVYKI 180  
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 248  
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 240  
QY 249 YQFFRIYLVNVTTHSNACSSKVAFYNEIFLSTAIISCVDLLLFFVGSGHWFQKIIIGLWN 308  
DB 241 YQFFRIYLVNVTTHSNACNSKVAFYNEIFLSTAIISCVDLLLFFVGSGHWFQKIIIGLWN 300  
QY 309 CVLCCR 313  
DB 301 CVLCCR 305  
RESULT 12  
ABP71378  
ID ABP71378 standard; protein; 305 AA.  
XX  
AC ABP71378;  
XX  
DR 28-APR-2003 (first entry)  
XX  
DE Human TGR343 protein.  
XX  
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;  
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotoxic;  
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;  
KW immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PN WO2003004678-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 01-JUL-2002; 2002MO-US020860.  
XX  
PR 03-JUL-2001; 2001US-0302800P.  
XX  
PA (TULA-) TULARIK INC.  
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;  
DR WPI: 2003-210368/20.  
DR N-PSDB; AB259171.  
XX  
PT New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
PT nephrolithiasis.

XX Claim 17; Page 62; 74pp; English.  
PS  
XX  
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides  
CC designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR38 end encoding  
CC polynucleotides. The polypeptides can be expressed by standard DNA  
CC recombinant methodology. The polypeptides are useful for screening or  
CC identifying modulators of GPCR or signal transduction. The modulators of  
CC signal transduction are useful for treating or preventing TGR-associated  
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
CC polypeptides are useful as targets for diagnosing or treating e.g.  
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,  
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
CC cirrhosis, lesions, jaundice, poriasis, lupus erythematosus, or acute  
CC inflammatory dermatoses. The present sequence represents a human TGR343  
CC protein  
XX  
SQ Sequence 305 AA;  
XX  
XX  
Query Match 96.9%; Score 1587; DB 6; Length 305;  
Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MPEHNTSRNNSCDPIVTPHILISLYFYVLIGLVGVISILFLVKNTRSVTTMAVINLVV 68  
DB 1 MPEHNTSRNNSCDPIVTPHILISLYFYVLIGLVGVISILFLVKNTRSVTTMAVINLVV 60  
QY 69 VHSVFLITVPPRLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128  
DB 61 VHSVFLITVPPRLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120  
QY 129 KDVVEFRKLAAVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYVYKI 188  
DB 121 KDVVEFRKLAAVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYVYKI 180  
QY 189 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSLSHOFMAQLKNLFFIGVILVCFEP 248  
DB 181 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSLSHOFMAQLKNLFFIGVILVCFEP 240  
QY 249 YQFPRFYLVNVTSHNACSSKVAFYNEIFLSTVAISCYDILLFVFGSHMFKOKIIGLWN 308  
DB 241 YQFPRFYLVNVTSHNACSSKVAFYNEIFLSTVAISCYDILLFVFGSHMFKOKIIGLWN 300  
QY 309 CVLCR 313  
DB 301 CVLCR 305  
RESULT 13  
AAO27265  
ID AAO27265 standard; protein; 305 AA.  
XX  
XX AAO27265;  
XX  
DT 17-SEP-2003 (first entry)  
XX  
DE Human G-protein coupled receptor GAVE18 protein sequence.  
XX  
XX Human G-protein coupled receptor; GAVE18; signal transduction;  
XX inflammation; physiological immunological response; anti-inflammatory;  
XX antiasthmatic; antirheumatic; antiarthritic; antisense therapy;  
XX chromosomal mapping; tissue typing; forensic biology;  
XX predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;  
XX rheumatoid arthritis.  
XX  
XX Homo sapiens.  
XX  
XX PN WO2003042399-A2.  
XX  
XX PD 22-MAY-2003.  
XX  
XX PF 08-NOV-2002; 2002WO-US035887.  
XX

PR 13-NOV-2001; 2001US-0354150P.  
PR 22-MAR-2002; 2002GB-00006891.  
XX  
XX (AVET ) AVENTIS PHARM INC.  
XX  
XX Bishngdtelo H, Cai J, Busch SJ, Gassenhuber J;  
XX  
XX WPI; 2003-457496/43.  
DR N-PSDB; AAL57070.  
XX  
XX  
PT New GAVE18 polypeptide and nucleic acid molecule encoding the  
PT polypeptide, useful for preventing and treating a disease or disorder  
PT associated with aberrant expression or activity of GAVE18, e.g. asthma or  
PT rheumatoid arthritis.  
XX  
XX  
PS Claim 7; Fig 6; 88pp; English.  
XX  
XX  
CC This invention relates to a novel G-protein coupled receptor (GAVE18)  
CC that is involved in signal transduction in respect to inflammation and  
CC the physiological immunological response. Molecules which may modulate  
CC the signalling activity or signal transduction of the receptor may be  
CC anti-inflammatory, antiasthmatic, antirheumatic or antiarthritic. The  
CC GAVE18 receptor and the DNA sequence encoding it may be a target for  
CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18  
CC proteins and antibodies may be useful in screening assays, detection  
CC assays (for example chromosomal mapping, tissue typing or forensic  
CC biology), or predictive medicine (for example diagnostic assays,  
CC prognostic assays, monitoring clinical trials and pharmacogenomics. The  
CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse  
CC agonist and antagonist are also useful for preventing and treating a  
CC disease or disorder associated with aberrant expression or activity of  
CC GAVE18, such as inflammation and immunological-related diseases or  
CC disorders, for example asthma, chronic obstructive pulmonary disease or  
CC rheumatoid arthritis. The present sequence is the amino acid sequence of  
CC the GAVE18 protein of the invention  
XX  
SQ Sequence 305 AA;  
XX  
XX  
Query Match 96.9%; Score 1587; DB 7; Length 305;  
Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MPEHNTSRNNSCDPIVTPHILISLYFYVLIGLVGVISILFLVKNTRSVTTMAVINLVV 68  
DB 1 MPEHNTSRNNSCDPIVTPHILISLYFYVLIGLVGVISILFLVKNTRSVTTMAVINLVV 60  
QY 69 VHSVFLITVPPRLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128  
DB 61 VHSVFLITVPPRLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120  
QY 129 KDVVEFRKLAAVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYVYKI 188  
DB 121 KDVVEFRKLAAVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYVYKI 180  
QY 189 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSLSHOFMAQLKNLFFIGVILVCFEP 248  
DB 181 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSLSHOFMAQLKNLFFIGVILVCFEP 240  
QY 249 YQFPRFYLVNVTSHNACSSKVAFYNEIFLSTVAISCYDILLFVFGSHMFKOKIIGLWN 308  
DB 241 YQFPRFYLVNVTSHNACSSKVAFYNEIFLSTVAISCYDILLFVFGSHMFKOKIIGLWN 300  
QY 309 CVLCR 313  
DB 301 CVLCR 305  
RESULT 14  
ADB78590  
ID ADB78590 standard; protein; 305 AA.  
XX  
XX ADB78590;  
XX

DT 04-DEC-2003 (first entry)  
 XX  
 DE Human G-protein coupled receptor GAVE18.  
 XX  
 KW human; GAVE19 orthologue; G-protein coupled receptor; GAVE18;  
 KW inflammatory disorder; immunological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003068803-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 13-FEB-2003; 2003WO-US004350.  
 XX  
 PR 14-FEB-2002; 2002US-0356686P.  
 XX  
 PR 22-AUG-2002; 2002GB-0001957A.  
 XX  
 PA (AVET ) AVENTIS PHARM INC.  
 XX  
 PI Bishngdrelo H, Dressler H, Cai J, Wright P;  
 XX  
 DR WPI; 2003-646474/61.  
 XX  
 PT New GAVE19 gene, useful for preparing a composition for treating  
 PT inflammatory or immunological disorders.  
 XX  
 PS Example 1; Fig 4; 76pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequence of the mouse  
 CC GAVE19 protein. Mouse GAVE19 is a G-protein coupled receptor which is the  
 CC orthologue of human GAVE18. The DNA and protein sequences of the  
 CC invention are useful for treating inflammatory and immunological  
 CC disorders. The present amino acid sequence represents the human GAVE18  
 CC protein.  
 CC  
 SQ Sequence 305 AA;  
 Query Match 96.9%; Score 1587; DB 7; Length 305;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;  
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 MEGHNTSRNSCDPIVTPHLISLYFVLIGLVGISILFLVKQNTS VTTMAVINLV 68  
 DB 1 MEGHNTSRNSCDPIVTPHLISLYFVLIGLVGISILFLVKQNTS VTTMAVINLV 60  
 QY 69 VHSVFLITVPRRLTYLIKKTMMFGLPFCRFVSAMLIHNYITFLPRVVLVTRYLIPFC 128  
 DB 61 VHSVFLITVPRRLTYLIKKTMMFGLPFCRFVSAMLIHNYITFLPRVVLVTRYLIPFC 120  
 QY 129 KQVEFFRGLAAVAAASAGKMTLVIVVPLVVSRYGIHEBYNEHCFFKHELAATYVXI 188  
 DB 121 KQVEFFRGLAAVAAASAGKMTLVIVVPLVVSRYGIHEBYNEHCFFKHELAATYVXI 180  
 QY 189 INMYTIVFIAVAVILVFOVEIIMLMVQKLRHSLISHOEFMAQIKNLFEGIVILVCELP 248  
 DB 181 INMYTIVFIAVAVILVFOVEIIMLMVQKLRHSLISHOEFMAQIKNLFEGIVILVCELP 240  
 QY 249 YQFFRIYINVTNTHSAGSSKVAFYNEITLSTATISCYLLLFVGGSGWPFQKTIIGLN 308  
 DB 241 YQFFRIYINVTNTHSAGSSKVAFYNEITLSTATISCYLLLFVGGSGWPFQKTIIGLN 300  
 QY 309 CVLCCR 313  
 DB 301 CVLCCR 305

DT 29-JUL-2004 (first entry)  
 XX  
 DE Human novel GPCR PGR13, SEQ ID NO:17.  
 XX  
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW kidney disorder; metabolic disorder; nutritive disorder; cancer;  
 KW ovary disorder; liver disorder; lung disorder; breast disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; anti-anemic;  
 KW cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antieborrheic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004040000-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 09-SEP-2003; 2003WO-US028226.  
 XX  
 PR 09-SEP-2002; 2002US-0409303P.  
 XX  
 PR 09-APR-2003; 2003US-0461329P.  
 XX  
 PA (PRIM-) PRIMAL INC.  
 XX  
 PI Galanaris GA, Bergmann UE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KU, Pavlova MN, Vassiliadis D, Zeng H;  
 DR WPI; 2004-390329/36.  
 DR N-PSDB; ADO28919.  
 XX  
 PT Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that mediate disease diagnosis and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 PS Claim 1; SEQ ID NO 17; 542pp; English.  
 XX  
 CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acid and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the



CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 8; Length 305;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;

Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	9	MPGHNTSRNSSCDPIVTPHILISLYFIYVIGLVGISILFLLVMQNTRSVTMAVINLAV	68
Db	1	MPGHNTSRNSSCDPIVTPHILISLYFIYVIGLVGISILFLLVMQNTRSVTMAVINLAV	60
Qy	69	VHSAVFLLTVPFRLTYLLIKKTMMFGLPFCFVSAMLHIMYLTFLFYVVLVTRYLIPFKC	128
Db	61	VHSAVFLLTVPFRLTYLLIKKTMMFGLPFCFVSAMLHIMYLTFLFYVVLVTRYLIPFKC	120
Qy	129	KDVEEFYRKLAHVAASAGMTLVIVIVPLVVSRYGIHEBYNEBCEKFKELAYTYVKI	188
Db	121	KDVEEFYRKLAHVAASAGMTLVIVIVPLVVSRYGIHEBYNEBCEKFKELAYTYVKI	180
Qy	189	INTMIVIFVLAVALVILVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFLP	248
Db	181	INTMIVIFVLAVALVILVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCFLP	240
Qy	249	YQFFRIYLVNVTSHSNACSSKVAFYNEIFLSVTAISCYDLLFVFGSHWFKOKIIGLMN	308
Db	241	YQFFRIYLVNVTSHSNACSSKVAFYNEIFLSVTAISCYDLLFVFGSHWFKOKIIGLMN	300
Qy	309	CVLCR 313	
Db	301	CVLCR 305	

Search completed: September 10, 2005, 10:07:03  
 Job time : 82 secs

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OM protein - protein search, using sw model

Run on: September 10, 2005, 10:03:32 ; Search time 23 Seconds

(without alignments)  
1309.385 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637

Sequence: 1 MQGCDPSPMGHNTSRNSSC.....GSHWFKQKTIIGLNCVLCR 313

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	13.6	391	2 A39297	somatostatin recep
2	221	13.5	391	2 A41795	somatostatin recep
3	221	13.5	391	2 C41795	somatostatin recep
4	220	13.4	344	2 T09508	inturin 17 purinerg
5	214	13.1	328	2 I38973	G protein-coupled
6	208	12.7	355	2 A55733	G protein-coupled
7	207.5	12.7	355	2 A45177	chemokine (C-C) re
8	207.5	12.7	356	2 I49340	MIP-1 alpha recept
9	206	12.6	369	2 JC2083	somatostatin recep
10	206	12.6	369	2 D41795	somatostatin recep
11	205	12.5	369	2 B41795	somatostatin recep
12	205	12.5	369	2 A45291	somatostatin recep
13	205	12.4	366	2 S29248	somatostatin recep
14	202.5	12.3	432	2 A43448	thrombin receptor
15	202	12.3	355	2 I49339	macrophage inflam
16	201.5	12.3	308	2 I50241	G protein-coupled
17	201.5	12.3	420	2 I51667	thrombin receptor
18	199	12.2	355	2 JQ1231	interleukin-8 rece
19	198.5	12.1	370	2 JC2549	heptahelical P2Y5-
20	197.5	12.1	380	2 UC2358	kappa opioid recep
21	197.5	12.0	425	2 A47249	brain-specific som
22	196	12.0	425	2 A37912	thrombin receptor
23	196	12.0	428	2 A44021	somatostatin recep
24	195	11.9	362	2 S33733	G protein-coupled
25	194.5	11.9	380	2 UC2434	kappa opioid recep
26	194	11.9	355	2 UC04304	orphan G protein-c
27	194	11.8	388	2 JN0605	somatostatin recep
28	193.5	11.8	367	2 JC2421	opioid receptor ho
29	193.5	11.8	367	2 I49022	kappa opioid recep

30	193.5	11.8	367	2 I56520	G protein-coupled
31	193	11.8	355	2 UC9067	G protein-coupled
32	193	11.8	380	2 A55259	kappa opioid recep
33	192.5	11.8	355	2 G02436	chemokine (C-C) re
34	192	11.7	370	2 S43087	orphan opioid rece
35	191.5	11.7	380	2 A48827	kappa opioid recep
36	191.5	11.7	428	2 S30508	probable G protein
37	191	11.7	380	2 S36143	kappa opioid recep
38	190.5	11.6	384	2 UC4629	somatostatin recep
39	190.5	11.6	423	2 UC7677	allatostatin recep
40	189.5	11.6	333	2 I38974	G protein-coupled
41	189	11.5	373	2 JE0087	delta opioid recep
42	186	11.4	418	2 A46226	somatostatin recep
43	185.5	11.3	383	2 S55594	G protein-coupled
44	185	11.3	400	2 I56553	mu opiate receptor
45	184	11.2	392	2 S65693	opioid receptor mu

## ALIGNMENTS

## RESULT 1

A39297

somatostatin receptor - rat

N/Alternate names: probable G-protein-coupled receptor; SRIF receptor

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 09-Jul-2004

C/Accession: A39297; A45102; S20088

R/Meyerhof, W.; Pautz, H.U.; Schoenrock, C.; Richter, D.

DNA Cell Biol. 10, 689-694, 1991

A/Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor express.

A/Reference number: A39297; MIMD:92096119; PMID:161599

A/Accession: A39297

A/Molecule type: mRNA

A/Residues: 1-391 <MEY>

A/Cross-references: UNIPROT:P28646; GB:X62314; GB:X61630; NID:G56309; PIDN:CAA44193.1; i

A/Experimental source: brain

A/Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat

R.J.L., X.U., Forte, M.; North, R.A.; Rose, C.A.; Snyder, S.H.

J. Biol. Chem. 267, 21307-21312, 1992

A/Title: Cloning and expression of a rat somatostatin receptor enriched in brain.

A/Reference number: A45102; MIMD:93016064; PMID:1400442

A/Accession: A45102

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-391 <L11>

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBI:P:116692)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 13.6%; Score 222; DB 2; Length 391;

Best Local Similarity 22.8%; Pred. No. 8e-11;

Matches 72; Conservative 75; Mismatches 119; Indels 50; Gaps 14;

QY	10	PGHNTSRNS-CDPIVTPHLIS-LYFIVLIGLVG--VISLFLVKNRNSVTTMAVI	64
DB	41	PGHNSQNGTLSEGGQSALISFIYSVCLVGLCGSNVIYILRYAKAKKT--ATNIYIL	98
QY	65	NLVVHVSFLLVPPFLTLTIKKTMFGLPCKFPASAMHIMHLYLFLVYVILVTRYLI	124
DB	99	NLAIDELMLSPVPLVISTLIRHWPFGALICRLVLSVDAVVMFYSIYCLTVLSVDRVVA	158
QY	125	PFCKDKVEFYRKLHVAASAGMTLVIVVPLV-STRYGHEEYNEBCEKFEKELAY	183
DB	159	VHPIIAARYRPTAKVNVNLGVWLSLIVLPIVFESTANS-GLYACMLMPEPQ	217
QY	184	TV-VKTIINMIV-FLVIAVAILLVQVFITMLMOKLSHLSHQEFAQIKN-----	235
DB	218	RMVGVFVLTPLMGFLIPGALICLY-----VLIIAKNR--NVALKAGQQRSEBRKIT	270
QY	236	---LRFIGVILVCLPYQFRIVYLVN-----VTHSNACSSKVAF-----	272



[illegible]

## RESULT 5

G:protein-coupled receptor 7 - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C:Accession:138973  
R:O'Dowd, B.F., Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;  
Genomics 28, 84-91, 1995  
A:Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like  
A:Reference number: A57647, MUID:96070436, PMID:7590751  
A:Accession:138973  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Releases: 1-328 <RES>  
A:Cross-references: UNIPROT:P48145, EMBL:U22491, NID:g953332, PIDN:AAC50197.1, PID:g95332  
C:Genetics:  
A:Gene: GDB:GPR7  
A:Cross-references: GDB:371714; OMIM:600730  
A:Map position:10q11.2-10q21.1  
C:Superfamily: vertebrate rhodopsin  
/Keywords: G protein-coupled receptor

Query Match	13.1%	Score 214;	DB 2;	length 328;
Best Local Similarity	21.2%;	Pred. No. 3.1e-10;		
Matches 61; Conservative	66;	Mismatches 125;	Indels 36;	Gaps 9;

QY PGHNTSRNSCCDPYATPHLIS---LYFVLIGLGVGISILFLVKM--NRSVYTMVAIV 65  
Db PALCSNASTIAPLPAPPLAAVAVPVYAVICAVGLAGNASAVLYTLDRPRKMTYNNLFTLN 78  
QY LVVVHVSPELLTPRELTYLLIKKTMPFGHLPFKCVSAMLHIMLYTLFELYVILVTRYLIF 125  
Db LAIDELFTVLPLINIDFLLRQMPFGELMCKLIVAIQYVTFSSLYFLTWSADRYLV 138  
QY FKCDKXVEFYRKLH--AVAAAGMVLTYIVVFLVNVSRIGIHEHYNEHC-FYFKHOLA 182  
Db LATESRRVAGRTSAPAPASLAWGIVTLVLPFAVA-RLDEQGRQCVLPQPEA 197  
QY YTYVKKINMYIVI-FVIAVAVILLVQVFIIMLVOKLHSLHSLOEFTMAOLK----- 235  
Db FMMRASRLTYLVDFAIPVSTICVLTYLLORLHAMELD-----SHAALBEAKRGRVFLV 253  
QY LFFLGVLVLPFLPYQFRI-----YYLVNVTHSNAC 266  
Db VALIAVCLLCWTMPHLSLTVALTDLDPOTPLVIAISYFITSLYTANSG 301

## RESULT 6

G:protein-coupled receptor GPR1 - human  
C:Species: Homo sapiens (man)  
C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A55733  
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heider, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.  
Genomics 23, 609-618, 1994

A>Title: Cloning of human genes encoding novel G protein-coupled receptors.  
 A|Reference number: A55733; MUID:95154831; PMID:7851889  
 A|Accession: A55733  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-355 <MAR>  
 A|Cross-references: UNIPROT:P46091; GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g57741  
 C|Genetics:  
 A|Gene: GDB:GPR1  
 A|Cross-references: GDB:371707; OMIM:600239  
 A|Map position: 15q25-15q26.1  
 C|Superfamily: vertebrate rhodopsin  
 C|Keywords: G protein-coupled receptor  
  
 Query Match 12.7%; Score 208; DB 2; Length 355;  
 Best Local Similarity 25.4%; Pred. No. 1e-09;  
 Matches 77; Conservative 53; Mismatches 101; Indels 72; Gaps 15;

Query Match	12.7%	Score 208	DB 2	length 355
Best Local Similarity	25.4%	Pred. No. 1e-09		
Matches 77	Conservative 53	Mismatches 101	Indels 72	Gaps 15

## 2

```

Oy      84  L-ICKTWAMFGLPCKCFVSAMLIHHVYTLFYVYILVTRYLIIFPKCKQKVEFYRKJAHVA  142
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      97  VANNFHHFPGTWLCKASFTQAQMMFSAVFELYISLDHYI-----HLIHFVL  144
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      143  ASAGMM---TLVIYIVPVLVSRGIMBEY-----NEHC--FKFH-----KEL  181
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      145  SHRRRTLNKSLIVLIETWLLASLLGGPALYFRDVEFNNHTLCYNNFQKHDPDLTLIRH  204
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      182  AYTIVK-IINMYIVIAVAVALLVQVILIMLMOKLRSLSHQEFMAQLKNLFEIG  240
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      205  VLTWVKEELIGLPLMLTMSICYLCILFEKV-----KKTIVLTSSRFMT---ILVVVV  253
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      241  VIILCFPLPYQEFRIYVIANVWTHSACSKV-----AFNBIPLSTATISCYDYL  289
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      254  AFVVCMPFMYHLSFWELTI--HNSYHHWMOAGIPLSTGLAFIN-----SLANPI  302
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      290  LFLV 292
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      303  LYV 305
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 7  
A45177  
chemokine (C-C) receptor 1 - human  
N/Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: A45177; I55671  
R/Neote: K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

## A; Refere:

A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-355 <NEO>  
A:Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDD:AAA36543.1; PID:g29241  
A:Experimental source: H660 cells  
A>Note: Sequence extracted from NCBI backbone (NCBIP:124876)  
R:Gao, J.  
J. Exp. Med. 177, 1421-1427, 1993  
A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha  
A:Reference number: I55671; MUID:93240122; PMID:7683036  
A:Accession: I55671  
A:Status: preliminary/ translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-355 <RES>  
A:Cross-references: GB:L10918; NID:g292416; PIDD:AAA36543.1; PID:g292417  
C:GeneticCB:  
A:Gene: GDB:CMKBR1; CMKR-1  
A:Cross-references: GDB:138446; OMIM:601159

Db 93 DYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFIFITLLTIDRYLAVVHVVFAALRAVTVF-- 150

Qy 138 LHAVALASAGMTLVIVIVPLVVSRYGIHNEYNEHCFFHKELAYTY----- 185

RESULT 10  
D41795

FT NON TER 1 1  
 FT NON TER 152 152  
 SQ SEQUENCE 152 AA; 18091 MW; B6B1416A57EC7582 CRC64;  
 Query Match 48.1%; Score 787; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-42;  
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 76 TVPRRLVYLTKKTMFGLPCKEPIVSAMLHIMYITLPYVYILVTRVLIPKCKOKVEFY 135  
 DB 1 TVPRRLVYLTKKTMFGLPCKEPIVSAMLHIMYITLPYVYILVTRVLIPKCKOKVEFY 60  
 QY 136 RKLHVAASAGMTLVIVIVPLVVSXGHEEYNEHCFFKHELYTYVKIINWIVI 195  
 DB 61 RKLHVAASAGMTLVIVIVPLVVSXGHEEYNEHCFFKHELYTYVKIINWIVI 120  
 QY 196 FVIAVAVILLVQVFIIMLVQKLRHSLSHQ 227  
 DB 121 FVIAVAVILLVQVFIIMLVQKLRHSLSHQ 152  
 RESULT 5  
 080UC5 PRELIMINARY; PRT; 131 AA.  
 ID 080UC5;  
 AC 080UC5;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE G protein-coupled receptor POR13 (Fragment).  
 GN Name=Gpr141;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1 TaxID=10090;  
 RN [1]  
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;  
 RA Vasiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.B.,  
 RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,  
 RA Bergman J.B., Galanakis G.A.;  
 RT "The G protein-coupled receptor repertoires of human and mouse.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).  
 DR EMBL: AY255553; AAO85065.1; -  
 DR MGD: MGI:2672983; Gpr141.  
 DR GO: GO:0004872; F:receptor activity; IRA.  
 KW Receptor.  
 FT NON TER 1 1  
 FT NON TER 131 131  
 SQ SEQUENCE 131 AA; 15261 MW; 58089C0AF5490DE1 CRC64;  
 Query Match 33.4%; Score 547; DB 2; Length 131;  
 Best Local Similarity 78.7%; Pred. No. 1.5e-27;  
 Matches 100; Conservative 13; Mismatches 14; Indels 0; Gaps 0;  
 QY 186 VKIINWIVFVIAVAVILLVQVFIIMLVQKLRHSLSHQEFMOKLFFIGVILVC 245  
 DB 5 VKIINWIVFVIAVAVILLVQVFIIMLVQKLRHSLSHQEFMOKLFFIGVILVC 64  
 QY 246 FLFYPQFRIRYLVNVVHNSNACSKVAFYNEIFLVTALSCYDILLFVFGSHVFKQKITG 305  
 DB 65 FLFYPQFRIRYLVNVVHNSNACSKVAFYNEIFLVTALSCYDILLFVFGSHVFKQKITG 124  
 QY 306 LAMCVIC 312  
 DB 125 MAMCLJC 131  
 RESULT 6  
 08BLT7 PRELIMINARY; PRT; 299 AA.  
 ID 08BLT7;  
 AC 08BLT7;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length  
 DE enriched library, clone:A530095019 product:hypothetical Rhodopsin-like  
 DE GPCR superfamily containing protein, full insert sequence.  
 GN Name=A530095019Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1 TaxID=10090;  
 RN [1]  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RX MEDLINE=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RX MEDLINE=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RX MEDLINE=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Kanno H., Akiyama J., Nishii K., Katsunai T., Taahiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,  
 RA Tameda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RX MEDLINE=C57BL/6J; TISSUE=Aorta and vein;  
 RX MEDLINE=C57BL/6J; TISSUE=Aorta and vein;  
 RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kaishiwagi K.,  
 RA Katoh H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shikata T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK041317; BAC30904.1; -  
 DR MGD: MGI:2441809; A530095019Rik.  
 DR GO: GO:0016021; C:integral to membrane; TMS.  
 DR GO: GO:0004930; F:G-protein coupled receptor activity; TMS.



DR GO:0007186; P-g-protein coupled receptor protein signalin. . .; TAS.  
DR InterPro: IPR000276; GPCR Rhodopsin.  
DR InterPro: IPR002286; P2\_purinocptor.  
DR PRINTS; PR01157; P2YPRNOCPTR.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEPTOR\_FL\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 299 AA; 34594 MW; D793823AF030E67D CRC64;

Query Match 32.5%; Score 532; DB 2; Length 299;  
Best Local Similarity 37.1%; Pred. No. 2.5e-26;  
Matches 104; Conservative 66; Mismatches 104; Indels 6; Gaps 4;

QY 20 CDPIVTPHLSLYFIVLIGLVGVISILFLVKNTRSVTMAVINLVVHVSFLLTVPF 79  
DB CDHCAKALITTAYSVVFPGVGTVMHMFKNQCSMIATIIINIVHSLILSLDF 83  
QY 80 RLTYLIKATWMLPFCCKFVSAMLIHMYITLFLFYVILVTRYITLFFPKCKDKVEFRKIH 139  
DB RLSTYSAVWKGSFTCRWVSGVYGHMYITLFLFYAIVTLRLIYFK-KLQMOQLQKH 142  
QY 140 AVAASAGMTLVIVIVVPLVSVRGYHEEYNE-EHCFKFKELAYTVYKIIINMIVIFI 198  
DB AVALSTIITVWTSFIFLPIFLPGYDPSYTEQRCFEPFKSLNSRDIIINISITIVM 202  
QY 199 AVAVILVFOVFIIMLVOKLRHSLSHOEFMVAKNLFFIIGVILVCPYOFRIYYP- 257  
DB TTYLLFLQMAVITLILKAYWPDMAHGEYRQIISFFFLVIVVCFIPHAFRVYFIQ 262  
QY 258 NVVTHSNACSSKVAFFNEIFLSTVTAISCYDLLIFVFGSH 297  
DB NPPEQEN---SKLIYNEICVALTAPCDMLCFIGGVII 299

## RESULT 7

ID 06XCE1 PRELIMINARY; PRT; 381 AA.  
AC 06XCE1;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE G-protein-coupled receptor GPR34.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
NC NCBT\_Taxid=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
R4 MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;  
RA Schulz A., Schoneberg T.;  
RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";  
RL J. Biol. Chem. 278:35531-35541(2003).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AY241090; AAP0429.1; -.  
DR GO:0016021; C:integral to membrane; IEA.  
DR GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.  
DR GO:0004872; F:receptor activity; IEA.  
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO:0007186; P-g-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR002276; GPCR Rhodopsin.  
DR InterPro; IPR002286; P2\_purinocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PRINTS; PR01157; P2YPRNOCPTR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_FL\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEPTOR\_FL\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 381 AA; 43619 MW; E0837BA1FD29666A CRC64;

Query Match 16.9%; Score 277; DB 2; Length 381;  
Best Local Similarity 25.7%; Pred. No. 4.2e-10;  
Matches 81; Conservative 73; Mismatches 137; Indels 24; Gaps 11;

QY 14 TERNSSC---DPIVTPHLSLYFIVLIGLVGVISILFLVKN-TRSVTMAVINLVV 69  
DB TORNENCLEEDNALSFAISFYSVIFVGLGNITATLAFILCHKRSISQIVLLNVAIA 91  
QY 70 HSVFLVTFPRLTYLI-KRTWFGLPFCCKFVSAMLIHMYITLFLFYVILVTRYITLFFPKC 128  
DB DLLIFCFLPRLIYHISNNWFMGWLICKIVGTLEFYNNMYSIILLGISLDRYKINS 151  
QY 129 KDKVEFRKLAHVAASAGMTLVIVIVVPLVSVRGYHEEYNEBHCFKFKELAVT 184  
DB VARPFMULTTTSRVHICCIWMAVALGFSLVVPSLFR---SDISNSTLCFHYRNKKAM 207  
QY 185 YKIIINMIVIFVIAVAAILLVFOVFII-MLVOKLRHSLSHOEFMVAKNLFFIGVI 242  
DB TEALINMIVIMFVIVPFLILLISYKIAKNLKSIRKANPKNAYQOTARNSFTVLI 267  
QY 243 L-VCELPYOFRIYILNVVTHSNACSSKVAFF-NEIFLSTVTAISCYDLLIFVFGSHW 298  
DB FTVCFVPMHMFVYVITSQIQNPSCYWKGIHTCNEMVLIFSSFNSCIDPVWY-FLMSSS 326  
QY 299 FKQKTIIGLMNCLCR 313  
DB 327 VAKTVLQIOL---ICR 337

## RESULT 8

ID 06XCB2 PRELIMINARY; PRT; 378 AA.  
AC 06XCB2;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE G-protein-coupled receptor GPR34 type 1.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Acanthomorphia; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
NC NCBT\_Taxid=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
R4 MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;  
RA Schulz A., Schoneberg T.;  
RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";  
RL J. Biol. Chem. 278:35531-35541(2003).  
CC EMBL; AY241119; AAP04328.1; -.  
DR GO:0016021; C:integral to membrane; IEA.  
DR GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.  
DR GO:0004872; F:receptor activity; IEA.  
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO:0007186; P-g-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR002276; GPCR Rhodopsin.  
DR InterPro; IPR002286; P2\_purinocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PRINTS; PR01157; P2YPRNOCPTR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_FL\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEPTOR\_FL\_2; 1.  
KW Receptor.  
SQ SEQUENCE 378 AA; 42747 MW; 9B8071FD348B3A86 CRC64;

Query Match 16.0%; Score 262; DB 2; Length 378;  
Best Local Similarity 28.9%; Pred. No. 3.7e-09;  
Matches 90; Conservative 62; Mismatches 133; Indels 26; Gaps 14;

QY 7 PMPGHNTSRNSSC---DPIVTPHLSLYFIVLIGLVGVISILFLVKNTRSVTMAV 63  
DB PSTPQH-INHSQCHQEDENLRPLAAMSLPFFVGLVGNLALAWFLQRSSNNLRFL 72  
QY 64 INLVVHVSFLLTVPRLTY-LIKKTWFGLPFCCKFVSAMLIHMYITLFLFYVILVTRY 122  
DB INCAVADVLLGCLPFRISYHNLNGDQMHGLPACMKVGNLFYNNMYSIMILGFISLHY 132

Qy 123 LIFEKCD-----KVEFYRKLHAAVAASAGMTLVIVVPLVSVRGHEEYNEHC 174  
Db 133 L-RIKGGRAROGITVTLGLGRCPWSVACGTMISLSLVLGIVPMV--AEDEHSNKC 188  
Qy 175 FKFEKELAYTVK--INMVIYFVIAVAVILLVPOVFLI--MLMVOQLRHSLSHQEFMA 231  
Db 189 FQFMGRSGNGKGAIFVVLVVFVFMVLVFMVLVSVYKIASKLRLVSDKDLPMARHYOR 248  
Qy 232 QLNKLFPI-GVILVCLPYOFR-IYYLVNVTSHNACS--SKVAFNEIFLSTAI-SCY 286  
Db 249 SAKSFVFLFVLCFPGPYHAFRPVYIFYOIKNNQPCPIIOMVARTNEIMLLSAFNSCL 308  
Qy 287 D-LILFVFGCS 296  
Db 309 DPVWYFLLSGS 319

## RESULT 9

Q6XCES PRELIMINARY; PRT; 359 AA.  
AC Q6XCES; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE G-protein-coupled receptor GPR34 (Fragment).  
OS Martes foina (Beach mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
OC Martes.  
OX NCBI\_TaxID=9659;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;  
RA Schulz A., Schoneberg T.;  
RT "The structural evolution of a P2Y-like G-protein-coupled receptor."  
J. Biol. Chem. 278:35531-35541(2003).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL: AY241086; APO4295.1; -  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . . ; IEA.  
DR InterPro: IPR002286; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm.1; 1-  
DR PRINTS: PR00237; GPCRHOOPSN.  
DR PRINTS: PR01157; P2YPRNOCPTR.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
FT NON TER 359  
SQ SEQUENCE 359 AA; 40780 MW; 9FC46DAE79B41244 CRC64;

Query Match 15.5%; Score 254.5; DB 2; Length 359;  
Best Local Similarity 23.5%; Pred. No. 1.1e-08;  
Matches 72; Conservative 77; Mismatches 136; Indels 21; Gaps 11;

Qy 7 BSMRGHTSRNSSC---DPIVTPHLISLYFIVLIGLVGVISILFLVKNK-TRSYTMA 62  
Db 43 PNPQGITATPNGTCPEMDKLLSLTISYVIPVGLVGNIALYVFLGIHRRNSTQIY 102  
Qy 63 VINLVVHVSFLLTVPRFLTLYIKKT-AMFGLPCKEVSAMLIHMYLTFLFYVILVTR 121  
Db 103 LNVALLADLLILPCLPRIMYHNRNQTGLVILCKVGLTFPMNYISIIILGFSIDR 162  
Qy 122 YLIFPKCKDVEFYRKL--HAAVASAGMTLVIV-IVPLVSVRGHEEYNEHC 177  
Db 163 YI---KINRSIOORRAVTRKQSIYVCTVTVALLAGPSAMITLLKGNH---NSTVC 216  
Qy 178 HKELAYTVYKINMVIY--FVIAVAVILLVPOVFIIMLVQGLRHSLSHQEFMAQLK 235

Db 217 RENNKAKEAIFPVVAVVWFVFLFLLIISYIKGKGLGISKRKSPFGSKYATARN 276  
Qy 236 LFPIGVIL-VCLPYOFRILYLVNVTSHNACS SKVAFY--NEIFLSTAI-SCYDLLE 291  
Db 277 SFVLLIFVLCFPGPYHAFRPVYISQLNSPSCVWKEIIHKXNEIMLVFSPNSCLDPV 336  
Qy 292 VFGGSH 297  
Db 337 FLMSN 342

## RESULT 10

Q7ZZA4 PRELIMINARY; PRT; 347 AA.  
AC Q7ZZA4; 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DE SI: b2462.9 (Novel protein similar to nucleotide receptors).  
GN Name=b2462.9, Synonyms=SI: b2462.9, SI: 2545;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Skuce C.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL590151; CAD6067.1; -  
DR ZFIN: ZDB-GENE-030616-77; pr2y41.  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . . ; IEA.  
DR InterPro: IPR002276; GPCR\_Rhodopsn.  
DR InterPro: IPR000018; P2Y\_Purinoceptor.  
DR Pfam: PF00001; 7tm.1; 1-  
DR PRINTS: PR00237; GPCRHOOPSN.  
DR PRINTS: PR01066; P2YPRNOCPTR.  
DR PRINTS: PR01157; P2YPRNOCPTR.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F83CC283E2 CRC64;

Query Match 15.3%; Score 250; DB 2; Length 347;  
Best Local Similarity 24.5%; Pred. No. 2e-08;  
Matches 81; Conservative 67; Mismatches 124; Indels 58; Gaps 14;

Qy 9 MEGHNTSRNSSC-----DPIVTPHLISLYFIVLIGLVGVISILFLVKNK-TRSYTMA 62  
Db 1 MPWSSKEVNPSCFPEDEEFTYILP--VSYSLVCFELINSVALMWFTTKMPKPSYV 58  
Qy 63 VINLVVHVSFLLTVPRFLTLYIKKT-AMFGLPCKEVSAMLIHMYLTFLFYVILVTR 121  
Db 59 MPTLALSDTLVYLSLPMILYYVANSNHPGVGLCKIVAFLYANLYCSILFLTCSVNR 118  
Qy 122 YLIFPKCKDVEFYRKLHAAVAASAGMTLVIVVPLV--SRG---IHEEYNEH 173  
Db 119 YLIGCHPISLTILIKRHAHMYCGFWTAVIACLVPTLLVNTSRGNSLTLCGDSRPE- 177  
Qy 174 CFKEKELAYTVYKINMVIYFVIAVAVILLVPOVFIIMLVQGLRHSLSHQEFMA 230  
Db 178 --EFNFVTYNSV---VNVLLIFLFVLIYVY---CLMARLDCORKGLAQOQSS 226  
Qy 231 AOLKMLFPIGVILV---CELPYOFER-IYY-----LVNVTSHNACS SKVAFY 274  
Db 227 SRKSKIKLIVLVVPAIGFVPHITRILTYAVRIFDADCKTLNIVNFSYKILTRPLASV 286



```
CC and heart.
CC -1- MISCELLANEOUS: Selective antagonists, such as montelukast
CC (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are
CC used in the treatment of the asthma crisis.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF119711; AAD42285.1; -.
DR EMBL; AF133266; AAD42778.1; -.
DR EMBL; AY424230; AAO92297.1; -.
DR HSSP; P34966; 1DDO.
DR Genew; HGNC:17451; CYSLTR1.
DR MIM; 300201.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004974; F:leukotriene receptor activity; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
DR InterPro; IPR004071; CysLeuX_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CYSTRCEPT.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 28
FT TRANSMEM 29 49
FT TRANSMEM 50 57
FT TRANSMEM 58 78
FT TRANSMEM 79 106
FT TRANSMEM 107 127
FT TRANSMEM 128 141
FT TRANSMEM 142 162
FT TRANSMEM 163 193
FT TRANSMEM 194 214
FT TRANSMEM 215 230
FT TRANSMEM 231 251
FT TRANSMEM 252 276
FT TRANSMEM 277 297
FT TRANSMEM 298 337
FT DISULFID 36 173
FT CARBOHYD 6 6
FT CARBOHYD 169 169
FT CARBOHYD 180 180
FT CARBOHYD 262 262
SQ SEQUENCE 337 AA; 38541 MW; B9B53940F895F245 CRC64;

Query Match 15.0%; Score 246; DB 1; Length 337;
Best Local Similarity 21.9%; Pred. No. 3.5e-08;
Matches 68; Conservative 81; Mismatches 133; Indels 28; Gaps 11;

QY 11 GHNTSRSSG-----DPIVPHLSLYFYVLIGLVGIVSILFLVLR-MNTRSVTTMAVIN 65
DB 5 GNLTSSATCDHRTIDFERNQVSTLVSMSISVGFPGNGFVLVYLITVYHKKSAPQYUYN 64
QY 66 LVVHVSFLTVPRLTYLTKK-TMMGSLPCKEVSAMLHHMYLFLPVVVLVTRYL 124
DB 65 LAVADLLCVCTLPRLRVVYTHKGIWLPGBDLCLSLTALVYNLYCSIFFTTA-----NS 118
QY 125 FPKC-----KDKVEFYRKLAHVAASGWTLLVIVVPLVVSRYGHEEYNEHCFTK 178
DB 119 FFKCIAIVFVQNIINIVTQKKAFVCGIWFIVILSSPFLMAK-PQCKKNTKCFEPP 177
QY 179 KE-LATTVYKINY--MIVFVIAVAVILLVQVFIIMAVQKLRSHSLSHOEFAQLQK 235
```

```
DB 178 QDNQTKNHLVLAHVSLSLVEFIIIPVYITVCTMILTLTKSKMKNLSSHKAIGMT-- 235
QY 236 LPEFIVILVCPYPGFRIYVNV-THSNAGSKVAFYNEIFLSTALS--CYDLLIF 291
DB 236 MVYTAFLVSPFPHYQRTIHLHFLHNEKPCDSVLRMKSVITLSTLAASNCFFPLLY 295
QY 292 VFGSGHWPQ 301
DB 296 FFGSGNFRKR 305

RESULT 13
Q6KCE7 PRELIMINARY; PRT; 373 AA.
AC Q6KCE7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G-protein-coupled receptor GPR34.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M30346200;
RA Schnitz A., Schoneberg T.;
RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";
RJ J. Biol. Chem. 278:35531-35541(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY241083; AAP04292.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:intrigic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR0157; P2YRHOCPTR.
DR PRINTS; PR01157; P2YRHOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 373 AA; 42842 MW; BCF7PB8102F2CCB0 CRC64;

Query Match 15.0%; Score 246; DB 2; Length 373;
Best Local Similarity 22.6%; Pred. No. 3.8e-08;
Matches 73; Conservative 82; Mismatches 132; Indels 36; Gaps 13;

QY 4 CDPFEN-----FGHTSR-----SSG-----DPIVPHLSLYFYVLIGLVGIVSILF 48
DB 10 GSPPGHFTINDSDVSNQFSGSVNVTSCPMDEKLSLVLTFTFYVIFVGLVGNITLY 69
QY 49 LVLKKN-TRSVTTMAVINLVVHVSFLTVPRLTYLTKK-TMMGSLPCKEVSAMLHH 106
DB 70 VFLGHRKNSIQIYLLANVAADLLIFCLPRFIMYHINQNRITGLVLCVGLTFYNN 129
QY 107 MYLTFVYVILVTRYLIFPKCKDVEFYRK--HVAASGWTLLV--VIVVPLV 160
DB 130 MYISILILGFSIDRYI--KINRISIQORRAITTKQSVYCCVVTVALAGFLTMILTL 186
QY 161 SHVYGHHEEYNEHCHEKELATVYKINMIV--FVIAVAVILLVQVFIIMVQK 218
DB 187 KKGG--HNSWTCCHYDKDNKAGEALFNFLVVMFLIFLLILSYIKGKNLRISK 242
QY 219 LRSHLSLHOFEAQKDNFFIGVIL-VCFLPYQFRIYVNVVTHSNAGSKVAFY--NE 275
DB 243 RSKSPNGSKVITTAHNSFIYVILIFTICFVPHARFPIYISSQLNASSCYMKEIHKNE 302
QY 276 IFLSVTAI-SCYDLLLFFVGSH 297
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Db 303 IMVLSSFNSCUDPVMTYFLMSSN 325

RESULT 14

CLT1 RAT STANDARD; PRT; 339 AA.

ID CLT1 RAT

AC Q92478;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cysteiny1 Leukotriene receptor 1 (CysLTR1).

GN Name=CysLTR1; Synonym=CysLTR1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OK NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,

RA Ohishi T., Soga T., Matsushima H., Furnichi K.;

RT "Characterization of cloned rat and porcine cysteinyl leukotriene

RT receptors."

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating

CC inflammation of the microvascular smooth muscle during an

CC inflammatory response. This response is mediated via a G-protein

CC that activates a phosphatidylinositol-calcium second messenger

CC system (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL: AB052685; BAB60825.1; -.

DR KGD, 619796; CysLTR1.

DR InterPro: IPR004071; Cysleuk\_receptor.

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR01533; CysLTRRECPTR.

DR PRINTS: PR00237; GPCRHOPOPSN.

DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; FALSE\_NEG.

DR PROSITE: PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 30

FT TRANSMEM 31 51

FT DOMAIN 52 59

FT TRANSMEM 60 80

FT DOMAIN 81 108

FT TRANSMEM 109 129

FT DOMAIN 130 143

FT TRANSMEM 144 164

FT DOMAIN 165 195

FT TRANSMEM 196 216

FT DOMAIN 217 232

FT TRANSMEM 233 253

FT DOMAIN 254 278

FT TRANSMEM 279 299

FT DOMAIN 300 339

FT DISULFID 98 175

FT CARBOHYD 6 6

FT CARBOHYD 171 171

SQ SEQUENCE 339 AA; 39143 MW; 281B41DF050DF8A CRC64;

Query Match 15.0%; Score 245.5; DB 1; Length 339;

Best Local Similarity 21.8%; Pred. No. 3.8e-08;

Matches 63; Conservative 79; Mismatches 122; Indels 25; Gaps 11;

QY 30 SLVFIVLIGLGVISILFLVK-MNTRSVTTMAVINLVVHVSVELLTPPRLTYLKK- 87

DB 30 TMYSMISVVGFGNSFVLVYLKTHKSAQVVMINLADLCVCLTPARVVYVYHKG 89

QY 88 TWMFGLPPCKFVSAMLHIMYTLFLFYVILVTRYLIFPKC-----KQKPEFRKLHAV 141

DB 90 KMFEGDFLCRLTYLTVALLVNLVCSIFEMTA-----MSFFRCVAIVFPQVINLVYQKAR 143

QY 142 AASAGMTLVIVIVPLVAVSRGIEHEEYNEHCEKFEHKE-LAYTVKIKINMIVV--FVY 198

DB 144 FVVCVIMFVILTVSSPFLSK-SYDEKQNTKCFEPPODKQTKVVLVHVSILFGYII 202

QY 199 AVAVILVFOVFIIIMAYQKLRHSLSHQEFMAQKMLFFIGVILVCFLPYQFPRIYYLN 258

DB 203 PFTVIVCYTMITLILKNMTKXNPSRKALIGM--IVVVAAPLVSMFPHIQALHILH 260

QY 259 VV-THSNACSSKVAFYNEIFLSVTAIS--CYDLILFVFGSHWFKKI 303

DB 261 FLHSETRSCDSVLRMQSKSVITLISLAAGNCDFDPLVYFSGGN-FRRRL 308

RESULT 15

ID Q6XCBI PRELIMINARY; PRT; 386 AA.

AC Q6XCBI;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE G-protein-coupled receptor GPR34 type 1.

OS Tetradodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoclestei;

OC Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetradodon.

OK NCBI\_TaxID=99883;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M30346200;

RA Schulz A., Schonberg T.;

RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";

RL J. Biol. Chem. 278:35531-35541(2003).

DR EMBL: AY241120; AAP04329.1; -.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G-. . .; IEA.

DR GO: GO:0048072; F:receptor activity; IEA.

DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO: GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro: IPR00276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCRHOPOPSN.

DR PRINTS: PR01157; P2PYRNOCPTR.

DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.

DR PROSITE: PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.

KW Receptor.

SQ SEQUENCE 386 AA; 43629 MW; 8CA737072E1C362 CRC64;

Query Match 14.9%; Score 244.5; DB 2; Length 386;

Best Local Similarity 25.2%; Pred. No. 4.8e-08;

Matches 79; Conservative 71; Mismatches 133; Indels 31; Gaps 14;

QY 7 PSMFHNTRSRNSG---DPIVTPHLISLYFVLIGLGVISILFLVKNMT-RSVTMA 62

DB 13 PSTPA-PINQPPPCAMDMLNRLPLATYISLFFISGLVGNLAALWVFLASGRNSMVF 71

QY 63 VINLVVHVSVELLTVPPRLTYLIR-KTWMFGLPPCKFVSAMLHIMYTLFLFYVILVTR 121

DB 72 LINCAVADLVLLACLPRIFFIHANGNQWLMSLACKVGVNLFYMMYISIMLALISLHR 131

QY 122 YLIFPKCKDKVBFYRKHLAV-----AASAGMTLVIVIVPLVAVSRGIEHEEYNE 171

DB 132 YL--KLRGGKAGQGRKRVITLMGRCPSPSWAACGLTMCLSVALVPMIVT--ABDKENS 185

QY 172 EHCEKEHELAYTYVK-IINMYIF--VIAVAVILVFOVFIIMVQKLRHSLSHOE 228  
Db 186 NOCFHFRRRSSNGKGAAPNALVLFWLVPATWPCYVKIASLLRVSRRPDLPNALR 245  
QY 229 FMAQLKULFPI-GVILVCFLEPYOPFRIYVL-NVVTSHNACSS--KVAFYNEIFLSTYAI- 283  
Db 246 YQSAKKSFFVLFLFVCFGPHAFRPPYIFVQMIHBNCTTLOMDQTNHVVLLLSAFN 305  
QY 284 SCYD-LLLFVFGGS 296  
Db 306 SCLDPVMVFFLLSGS 319

Search completed: September 10, 2005, 10:08:30  
Job time : 84 secs

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041 WONDERTHAT ANYTHING CAN BE FOUND IN THIS WORLD OF OURS

QY 309 CVCRC 313  
DB 301 CVCRC 305

## RESULT 2

Q7TOP0 PRELIMINARY; PRT; 305 AA.

DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)

DE G protein-coupled receptor 141.

GN Name=Gpr141.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;  
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,  
RA Schioth H.B.;

RT "Seven evolutionarily conserved human rhodopsin G protein-coupled  
RT receptors lacking close relatives.";

RL FEBS Lett. 554:381-388(2003).

DR EMBL; AY288432; AAP7214.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsn.

DR PROSITE; PS50262; G\_PROTEIN\_RECERP\_F1\_2; 1.

KM Receptor.

SQ SEQUENCE 305 AA; 35284 MW; 74C7EB210158D554 CRC64;

Query Match

Best Local Similarity 79.7%; Score 1304; DB 2; Length 305;  
Matches 247; Conservative 24; Mismatches 33; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLISLYFIVLIGLVGISILFLVKNKTRSVTMAVINLV 68  
1 MGEVNTSENSCDPIAHHLTSTYFIVLIGLVGISILFLVKNKTRSVTMAVINLV 60

DB 61 VHGVPFLTVPFRLAYLIGKWTFGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKR 120

QY 69 VHSVELTVPFRLTVIKKTMMGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKC 128  
1 VHGVPFLTVPFRLAYLIGKWTFGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKR 120

QY 129 KDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 188  
121 RDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 180

DB 189 INMYIVFVIAVAVILVQVFIIMLMVOKLRHSLLSHOFPMVQNLNLPFGIIVLCPFL 248  
181 INMYIVFVIAVAVILVQVFIIMLMVOKLRHSLLSHOFPMVQNLNLPFGIIVLCPFL 240

QY 249 YQFERYLVNVTHTSAACSSKVAFFNEIFLSTVAISCVLLLFVPGSGMWFQKIIGLNN 308  
241 YQFERYLVNVTHTSAACSSKVAFFNEIFLSTVAISCVLLLFVPGSGMWFQKIIGLNN 300

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
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QY 309 CVCRC 312  
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DB 309 CVCRC 312  
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QY 309 CVCRC 312  
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DB 309 CVCRC 312  
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QY 309 CVCRC 312  
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DB 309 CVCRC 312  
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DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DE G protein-coupled receptor 141.

GN Name=Gpr141;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;  
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,  
RA Schioth H.B.;

RT "Seven evolutionarily conserved human rhodopsin G protein-coupled  
RT receptors lacking close relatives.";

RL FEBS Lett. 554:381-388(2003).

DR EMBL; AY288432; AAP7214.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsn.

DR PROSITE; PS50262; G\_PROTEIN\_RECERP\_F1\_2; 1.

KM Receptor.

SQ SEQUENCE 247 AA; 28462 MW; A677E0011BFICE51 CRC64;

Query Match

Best Local Similarity 51.7%; Score 847; DB 2; Length 247;  
Matches 167; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLISLYFIVLIGLVGISILFLVKNKTRSVTMAVINLV 68  
1 MGEVNTSENSCDPIAHHLTSTYFIVLIGLVGISILFLVKNKTRSVTMAVINLV 60

DB 61 VHGVPFLTVPFRLAYLIGKWTFGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKR 120

QY 69 VHSVELTVPFRLTVIKKTMMGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKC 128  
1 VHGVPFLTVPFRLAYLIGKWTFGFLPCKFVSAMLIHMYLTFLLFYVILVIRYLIFFKR 120

QY 129 KDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 188  
121 RDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 180

DB 189 INMYIVFVIAVAVILVQVFIIMLMVOKLRHSLLSHOFPMVQNLNLPFGIIVLCPFL 248  
181 INMYIVFVIAVAVILVQVFIIMLMVOKLRHSLLSHOFPMVQNLNLPFGIIVLCPFL 240

QY 249 YQFERYLVNVTHTSAACSSKVAFFNEIFLSTVAISCVLLLFVPGSGMWFQKIIGLNN 308  
241 YQFERYLVNVTHTSAACSSKVAFFNEIFLSTVAISCVLLLFVPGSGMWFQKIIGLNN 300

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
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QY 309 CVCRC 312  
301 CVCRC 304

DB 309 CVCRC 312  
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QY 309 CVCRC 312  
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DB 309 CVCRC 312  
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QY 309 CVCRC 312  
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DB 309 CVCRC 312  
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DB 309 CVCRC 312  
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301 CVCRC 304

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301 CVCRC 304

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301 CVCRC 304

DB 309 CVCRC 312  
301 CVCRC 304

QY 309 CVCRC 312  
301 CVCRC 304

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2005, 03:07:41 ; Search time 27 Seconds  
(without alignments)  
865.376 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637  
Sequence: 1 MOKCDPSPMGHTSHNSSC.....GGSHPFKQKIGLNCVLGR 313

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	229	14.6	337	3	US-09-044-404A-2
2	232	14.6	337	4	US-09-586-924-2
3	232	14.2	381	4	US-09-745-842-21
4	231	14.1	358	3	US-08-988-876-3
5	231	14.1	358	4	US-09-919-172-22
6	223	13.6	346	4	US-09-585-876-2
7	221	13.5	391	1	US-07-816-283-2
8	221	13.5	391	1	US-07-816-283-2
9	221	13.5	391	1	US-08-417-103-4
10	221	13.5	391	1	US-08-417-103-4
11	221	13.5	391	1	US-08-417-103-4
12	221	13.5	391	1	US-08-417-103-4
13	219	13.4	344	2	US-09-826-509-569
14	219	13.4	344	2	US-08-467-948A-8
15	217.5	13.3	355	4	US-08-833-752-9
16	217.5	13.3	355	4	US-09-938-719-9
17	217.5	13.3	355	4	US-09-939-226B-9
18	216	13.2	391	3	US-08-120-601B-8
19	215	13.1	331	4	US-09-170-496D-36
20	214	13.1	325	2	US-08-467-948A-29
21	214	13.1	325	1	US-08-467-947A-29
22	214	13.1	328	1	US-08-148-215A-2
23	214	13.1	328	4	US-09-170-496D-12
24	214	13.1	328	4	US-09-170-496D-12
25	214	13.1	338	3	US-08-988-876-8
26	214	13.1	338	3	US-09-303-524A-2
27	214	13.1	338	4	US-09-745-842-13

28	214	13.1	338	4	US-09-919-497-77	Sequence 77, Appl
29	214	13.1	339	4	US-09-170-496D-182	Sequence 182, App
30	213	13.0	331	4	US-09-910-695-4	Sequence 4, Appl1
31	212.5	13.0	389	3	US-08-430-286A-7	Sequence 7, Appl1
32	211	12.9	369	4	US-09-826-509-571	Sequence 571, App
33	208.5	12.7	381	1	US-08-467-125-2	Sequence 2, Appl1
34	208.5	12.7	381	2	US-08-911-320A-2	Sequence 2, Appl1
35	208.5	12.7	381	3	US-09-217-101-2	Sequence 2, Appl1
36	208	12.7	331	4	US-09-170-496D-184	Sequence 184, App
37	208	12.7	335	4	US-09-170-496D-2	Sequence 2, Appl1
38	207.5	12.7	355	1	US-08-012-988A-2	Sequence 2, Appl1
39	207.5	12.7	355	1	US-08-450-393A-5	Sequence 5, Appl1
40	207.5	12.7	355	3	US-08-446-669-5	Sequence 5, Appl1
41	207.5	12.7	355	3	US-09-239-938-1	Sequence 1, Appl1
42	207.5	12.7	355	4	US-09-886-319A-14	Sequence 14, Appl1
43	207.5	12.7	355	4	US-10-039-659A-13	Sequence 13, Appl1
44	207.5	12.7	355	4	US-09-561-068-1	Sequence 1, Appl1
45	207.5	12.7	355	4	US-09-625-573-5	Sequence 5, Appl1

## ALIGNMENTS

RESULT 1  
US-09-044-404A-2

Sequence 2, Application US/09044404A  
Patent No. 6200775

GENERAL INFORMATION:

APPLICANT: SATHI, GANESH

APPLICANT: HALSEY, WENDY

APPLICANT: ELIS, CATHERINE

APPLICANT: AMES, ROBERT

APPLICANT: FOLEY, JAMES

APPLICANT: SARAU, HENRY

TITLE OF INVENTION: CDNA CLONE HMTF91 THAT ENCODES

TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: SmithKline Beecham Corporation

STREET: 790 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,404A

FILING DATE: MARCH 19, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/844,795

FILING DATE: APRIL 22, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T.

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: GH-70001-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-044-404A-2

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Query Match          14.6%; Score 239; DB 3; Length 337;
Best Local Similarity 21.6%; Pred. No. 7.8e-14;
Matches 67; Conservative 81; Mismatches 134; Indels 28; Gaps 11;

QY 11 GHNTSNSSC---DPIVPHLISLYFIYILGGLVGVISILFLVYK-MNTRSVTTMAVIN 65
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 5 GNLTVSSAATCHDITIDFERNQVSTLVSMTSVGFENGFLVLYLLIKTHKKSAPQVYMIN 64
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 66 LVVHVSVELLTVPEFRLTYLIK-K-TWMEGLPFCKFVSAMLHHMYLFLFYVILVTRYLI 124
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DB 65 LAVADLLCVCTLPRLRVVYVYHKGIMLFGDPLCKLSTYALYVNLVYCSIFPMTA-----MS 118
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 PFRC-----KDKVEFYRKLAHVAASAGMNTLVIIVPELVVSRVGIHEEYNEHCFFKH 178
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 119 FFRCLAIIVFPVQINIMLVTKKARFVCVGIWIFVILSSDFLMAK-PQKQKNTYKCFEPP 177
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 179 KE-LATVYKINY--MIVIFVIAVAVILLVPOVFIIMLVOKLRHSLSHOEFWAOLKN 235
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 178 QNQTGNHVLVHLYVSLFVGFILIPFVILICYTMILTLTKSKMKNLSSHKAIGMI-- 235
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 236 LFFIGVILVCELPYOFRIYILNV--THSNACSSKVAFYNEIFLSTALS---CYDLLLF 291
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 236 MVVTAFLVSFMPYHIOHTIHLFHNFTKPCDSVLRMQKSVVITLSLAASNCDFDPLLY 295
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 292 VEGGSHMFQ 301
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RESULT 2
US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SAHNE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PR
; ORGANISM: HOMO SAPIENS
US-09-586-924-2

Query Match          14.6%; Score 239; DB 4; Length 337;
Best Local Similarity 21.6%; Pred. No. 7.8e-14;
Matches 67; Conservative 81; Mismatches 134; Indels 28; Gaps 11;

QY 11 GHNTSNSSC---DPIVPHLISLYFIYILGGLVGVISILFLVYK-MNTRSVTTMAVIN 65
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 5 GNLTVSSAATCHDITIDFERNQVSTLVSMTSVGFENGFLVLYLLIKTHKKSAPQVYMIN 64
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 66 LVVHVSVELLTVPEFRLTYLIK-K-TWMEGLPFCKFVSAMLHHMYLFLFYVILVTRYLI 124
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 65 LAVADLLCVCTLPRLRVVYVYHKGIMLFGDPLCKLSTYALYVNLVYCSIFPMTA-----MS 118
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 PFRC-----KDKVEFYRKLAHVAASAGMNTLVIIVPELVVSRVGIHEEYNEHCFFKH 178
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 119 FFRCLAIIVFPVQINIMLVTKKARFVCVGIWIFVILSSDFLMAK-PQKQKNTYKCFEPP 177
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3
US-09-745-842-21
; Sequence 21, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-Dubridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopetex, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 381
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: G protein-coupled receptor 34; hugpr34
US-09-745-842-21

Query Match          14.2%; Score 232; DB 4; Length 381;
Best Local Similarity 21.5%; Pred. No. 3.8e-13;
Matches 66; Conservative 83; Mismatches 140; Indels 18; Gaps 9;

QY 5 DEPSMPGHNTSNSSC---DPIVPHLISLYFIYILGGLVGVISILFLVYK-MNTRSVTT 60
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 31 DQPFONFSAATPVVTTCPMDKELSLVLTTSYSVIFVIGLVGNIILVYFLGHRKRSIQ 90
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 MAVINLVVHVSVELLTVPEFRLTYLIK-K-TWMEGLPFCKFVSAMLHHMYLFLFYVILV 119
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 91 IYLLNVAIADLLILICLDFPRITWTHINQKMWILGVILCVGTLFYMANNYISILIGFISL 150
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QY 120 TRYLLPFCKDKVEFYRKLAHVAASAGMNTLVI--VIVPELVVSRVGIHEEYNEHCFFK 176
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 151 DRYIKINSIQQRKAITTKQSIYVCCIVMMALAGFLMILTLKKG---HNSWTCFH 206
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 177 FHKELATVYKINYMIY--FVIAVAVIILVFOVFIIMLVOKLRHSLSHOEFWAOLK 234
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 207 YRDKNNAKGEAIFNFIIVVMFMLFLILISYIKGKMLIRISKRSKRPSPGKATYAR 266
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 235 NLFIFGVLV--VCELPYOFRIYILNVVTHSNACSSKVAFY--NEIFLSTALV--SCYDLL 290
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 267 NSFIVLITFTICFVYHAFRIYISSQNLVSSCTWKEIVHKTNEIMLVLSFNSCLDPVM 326
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 291 FVFGGSH 297
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 327 YFLMSSN 333
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RESULT 4
US-08-988-876-3
; Sequence 3, Application US/08988876

```

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/ Patent No. 6063596
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Bandman, Olga
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Yue, Henry
/ TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
/ TITLE OF INVENTION: WITH IMMUNE RESPONSE
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/988,876
/ FILING DATE: Herewith
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0441 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: PROSTUT09
/ CLONE: 1650519
/ US-08-988-876-3

Query Match          14.1%; Score 231; DB 3; Length 358;
Best Local Similarity 24.3%; Pred. No. 4,4e-13;
Matches 76; Conservative 59; Mismatches 144; Indels 34; Gaps 10;

QY 10 PGNHTSRNSCDPIYTPHLISLYFI--VLIGLVGYSILFLVKNKNTSVTTMAVINLV 67
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 30 PGNHTLHNEFDPIVLPVLYLIFVASILNGIA-----VWIFPHIRNKTSPFIYKNTIV 84
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 68 VVHSVFLVTPPRLTYLIK-KTMMGELPRCKVSAHMLHTLFLFYVVIIVTRLIFF 126
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 85 VADLMTLTLPFRIVHADGFGPMYEFKILCRYTSVLFYANMTSYVFLGLISIDRYLKV 144
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 127 KCKDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGIIHEBYNEBHCFFKHELAITYV 186
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 145 KFGGSRMYSITFTKVLSCVAVIMAVLSLPMIILTNQPTEDNHDCKLSPLGVKNH 204
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 187 KIINMIVIFVAVAVIILVFOVFIIIMLVOKLRHSLSHQEFMAQLN-----LFF 238
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 205 TAVTYVNSCLFVAIVVILIGCYIAI-----SRVIHKSSROFISQSRKRKNOSIRVV 257
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 229 IGVILVCELPYQFPRFRI-----YLVNVTSHNACSSKVAFY-NELFISVTAIS-CYDLLLFV 292
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 258 VAVVTCFLPFLHLCRMPSTFPHLDRLDBSA--QKILVYCKEITFLSACNVCLDPIIYF 315
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 293 F---GGSWFKOK 302
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Db 316 FMCRSFSPMLFKK 328

RESULT 5
US-09-919-172-22
/ Sequence 22; Application US/09919172
/ Patent No. 6673545
/ GENERAL INFORMATION:
/ APPLICANT: Paris, Mary
/ APPLICANT: Turner, Christopher M.
/ TITLE OF INVENTION: PROSTATE CANCER MARKERS
/ FILE REFERENCE: PA-0036 US
/ CURRENT APPLICATION NUMBER: US/09/919,172
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/222,469
/ PRIOR FILING DATE: 2000-07-28
/ SOFTWARE: PERL Program
/ SEQ ID NO 22
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6673545 1650519CD1
/ US-09-919-172-22

Query Match          14.1%; Score 231; DB 4; Length 358;
Best Local Similarity 24.3%; Pred. No. 4,4e-13;
Matches 76; Conservative 59; Mismatches 144; Indels 34; Gaps 10;

QY 10 PGNHTSRNSCDPIYTPHLISLYFI--VLIGLVGYSILFLVKNKNTSVTTMAVINLV 67
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 30 PGNHTLHNEFDPIVLPVLYLIFVASILNGIA-----VWIFPHIRNKTSPFIYKNTIV 84
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 68 VVHSVFLVTPPRLTYLIK-KTMMGELPRCKVSAHMLHTLFLFYVVIIVTRLIFF 126
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 85 VADLMTLTLPFRIVHADGFGPMYEFKILCRYTSVLFYANMTSYVFLGLISIDRYLKV 144
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 127 KCKDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGIIHEBYNEBHCFFKHELAITYV 186
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 145 KFGGSRMYSITFTKVLSCVAVIMAVLSLPMIILTNQPTEDNHDCKLSPLGVKNH 204
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 187 KIINMIVIFVAVAVIILVFOVFIIIMLVOKLRHSLSHQEFMAQLN-----LFF 238
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 205 TAVTYVNSCLFVAIVVILIGCYIAI-----SRVIHKSSROFISQSRKRKNOSIRVV 257
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 229 IGVILVCELPYQFPRFRI-----YLVNVTSHNACSSKVAFY-NELFISVTAIS-CYDLLLFV 292
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 258 VAVVTCFLPFLHLCRMPSTFPHLDRLDBSA--QKILVYCKEITFLSACNVCLDPIIYF 315
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 293 F---GGSWFKOK 302
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 316 FMCRSFSPMLFKK 328

RESULT 6
US-09-585-876-2
/ Sequence 2; Application US/09585876
/ Patent No. 6586205
/ GENERAL INFORMATION:
/ APPLICANT: Glucksmann, Maria Alexandra
/ APPLICANT: Slios-Santiago, Immaculada
/ TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like molecule and
/ TITLE OF INVENTION: Uses Thereof
/ FILE REFERENCE: 5800-88
/ CURRENT APPLICATION NUMBER: US/09/585,876
/ CURRENT FILING DATE: 2000-06-01
/ EARLIER APPLICATION NUMBER: 60/182,061
/ EARLIER FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
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Db 271 LNWVVVVVFIWMP--FYVQLVNVFAEQDQATVSQLSVILGYSANCPILYGLSD 328  
QY 273 -YNEIFLSTVATSCYD 287  
Db 329 NFKRSFORILCLSMWD 344

## RESULT 13

US-08-467-948A-8  
Sequence 8, Application US/08467948A  
Patent No. 5998164  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR2  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-948A-8

Query Match 13.4%; Score 219; DB 2; Length 344;  
Best Local Similarity 27.1%; Pred. No. 5e-12;

Matches 75; Conservative 54; Mismatches 128; Indels 20; Gaps 12;

QY 31 LNFIVILGSLV-GVISILFLVKNRSTVTMAVINLVVHVSFLLTVPRRLTYLIKKTW 89  
Db 23 MFSWVFLGLISNCVAIYIFICVLKVRNRTTYMINLMSDLTFVFTLPFRIFYFTTRW 82  
QY 90 MFGLPCKEFSVAMLHIMVLTFLFYVVLIVTRYL-IFPKCKDKVEFRKLHVAASAGW 148  
Db 83 PFGDLCKISVWLFTYTMGSIILFTCTISVDRFLAIYVPRKKT-LRTKRNKIVCTGVM 141  
QY 149 TLVIIVVPLVVSRYGHEEYN--EEHCFKFKELAY-TYVKIINMYIVFVIAVAVIL- 204  
Db 142 LTVIGSAPAVFVQ-STHSGGNNAEACFENPPEATWTKYLS----RIVIFIEIVGFIP 196  
QY 205 LVEQVFIIMLVQKLRSL-LSHQEF-MAQLKNLFFIGVIL--VCPLPYGFPRIYIYNV 260

Db 197 LILNVYCSSMVLKTLRKPTVLSRSKINKKVLKMIHVHLIIFPCGCVPININILXSLR 256  
QY 261 THSNACSKVAFYNEIFLSTVTAIS---CYDLLFLVF 293  
Db 257 TQTFVNCVVAAVRTMYPIITLCIAVNCFCFDPVYVF 293

## RESULT 14

US-08-467-947A-8  
Sequence 8, Application US/08467947A  
Patent No. 6090575  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-947A-8

Query Match 13.4%; Score 219; DB 3; Length 344;  
Best Local Similarity 27.1%; Pred. No. 5e-12;

Matches 75; Conservative 54; Mismatches 128; Indels 20; Gaps 12;

QY 31 LNFIVILGSLV-GVISILFLVKNRSTVTMAVINLVVHVSFLLTVPRRLTYLIKKTW 89  
Db 23 MFSWVFLGLISNCVAIYIFICVLKVRNRTTYMINLMSDLTFVFTLPFRIFYFTTRW 82  
QY 90 MFGLPCKEFSVAMLHIMVLTFLFYVVLIVTRYL-IFPKCKDKVEFRKLHVAASAGW 148  
Db 83 PFGDLCKISVWLFTYTMGSIILFTCTISVDRFLAIYVPRKKT-LRTKRNKIVCTGVM 141  
QY 149 TLVIIVVPLVVSRYGHEEYN--EEHCFKFKELAY-TYVKIINMYIVFVIAVAVIL- 204  
Db 142 LTVIGSAPAVFVQ-STHSGGNNAEACFENPPEATWTKYLS----RIVIFIEIVGFIP 196



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 10, 2005, 07:21:37 ; Search time 75 Seconds

(without alignments)  
1646.094 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637  
Sequence: 1 MOKCDPSPMGHNTSRNSSC.....GGSHWRKQKIGLVNCLCR 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
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10: /cgn2\_6/ptodata/1/pubppa/US09B\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/1/pubppa/US10A\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubppa/US11A\_PUBCOMB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppa/US11B\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1637	100.0	313	14	US-10-085-233B-2
2	1634	99.8	313	16	US-10-467-252-4
3	1610	98.4	312	10	US-09-782-974C-82
4	1610	98.4	312	17	US-10-467-492A-82
5	1610	98.4	312	17	US-10-975-979-82
6	1610	98.4	367	16	US-10-467-252-6
7	1610	98.4	448	15	US-10-292-798-1008
8	1587	96.9	305	9	US-09-995-225-4
9	1587	96.9	305	10	US-09-995-225-4
10	1587	96.9	305	14	US-10-055-106C-2
11	1567	96.9	305	14	US-10-188-405-10

12	1587	96.9	305	14	US-10-293-171-2	Sequence 2, Appl1
13	1587	96.9	305	14	US-10-017-161-1194	Sequence 1194, Ap
14	1587	96.9	305	15	US-10-366-504-7	Sequence 7, Appl1
15	1587	96.9	305	15	US-10-297-908A-1	Sequence 1, Appl1
16	1587	96.9	305	16	US-10-467-252-5	Sequence 5, Appl1
17	1587	96.9	543	17	US-10-505-466-110	Sequence 110, App
18	1526	93.2	339	16	US-10-398-036-6	Sequence 6, Appl1
19	1141	69.7	269	14	US-10-366-504-2	Sequence 2, Appl1
20	548	33.5	149	10	US-09-782-974C-22	Sequence 22, Appl1
21	548	33.5	149	17	US-10-467-492A-22	Sequence 22, Appl1
22	548	33.5	149	17	US-10-975-979-22	Sequence 22, Appl1
23	249	15.2	337	14	US-10-290-078-21	Sequence 21, Appl1
24	247	15.1	337	14	US-10-167-191-6	Sequence 3, Appl1
25	247	15.1	337	15	US-10-400-991-6	Sequence 6, Appl1
26	246	15.0	337	9	US-09-866-230-8	Sequence 8, Appl1
27	246	15.0	337	9	US-09-828-478-5	Sequence 5, Appl1
28	246	15.0	337	10	US-09-991-225-6	Sequence 6, Appl1
29	246	15.0	337	14	US-10-055-106C-3	Sequence 3, Appl1
30	246	15.0	337	14	US-10-225-567A-547	Sequence 547, App
31	246	15.0	337	14	US-10-349-021-5	Sequence 5, Appl1
32	246	15.0	337	15	US-10-369-405-6	Sequence 6, Appl1
33	246	15.0	337	15	US-10-692-605-4	Sequence 4, Appl1
34	246	15.0	337	18	US-10-499-172-19	Sequence 19, Appl1
35	239	14.6	337	10	US-09-779-679-27	Sequence 27, Appl1
36	236	14.4	337	18	US-10-499-172-22	Sequence 22, Appl1
37	233	14.2	345	17	US-10-932-004-18	Sequence 18, Appl1
38	232	14.2	381	10	US-09-745-842-21	Sequence 21, Appl1
39	232	14.2	381	14	US-10-225-567A-414	Sequence 414, App
40	232	14.2	381	16	US-10-473-127-1417	Sequence 1417, Ap
41	232	14.2	381	16	US-10-473-127-1418	Sequence 1420, Ap
42	232	14.2	381	16	US-10-473-127-1420	Sequence 1421, Ap
43	232	14.2	381	16	US-10-473-127-1421	Sequence 1423, Ap
44	232	14.2	381	16	US-10-473-127-1423	Sequence 1425, Ap
45	232	14.2	381	16	US-10-473-127-1425	

## ALIGNMENTS

RESULT 1  
US-10-085-233B-2  
; Sequence 2, Application US/10085233B  
; Publication No. US20030087249A1  
; GENERAL INFORMATION:  
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA  
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR  
; FILE REFERENCE: MPI2001-021PRCP1M  
; CURRENT APPLICATION NUMBER: US/10/085,233B  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/272,677  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-085-233B-2

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DB	1	MOKCDPSPMGHNTSRNSSCDPIVTPHILSYLFIIVIGLVGVISILFLVVMNTRSVTT	60
QY	61	MAVINLVVHVSFLLTVPRLLTYLLIKTWMFGLPCKEVSAMTHIMYLLTFEYVILVT	120
DB	61	MAVINLVVHVSFLLTVPRLLTYLLIKTWMFGLPCKEVSAMTHIMYLLTFEYVILVT	120
QY	121	RYLIFFKCKDKVEFYRKJLHANAASAGMTLVIVIVPLVVSRYGJHEEYNEBCKRFHKE	180

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Db 181 LATVYKTIINMIVIVFAVAIVLLVPOVEITMLMVKLRSHLSHOEFMAQLKXLPFLIG 240
QY 241 VILVCELPYQPFRIYYLNVVTHSNACSSKVAFYNEIFLSTVAISCYDLLFPVGGSHWPK 300
Db 241 VILVCELPYQPFRIYYLNVVTHSNACSSKVAFYNEIFLSTVAISCYDLLFPVGGSHWPK 300
QY 301 OKIIGLMNCVLCR 313
Db 301 OKIIGLMNCVLCR 313

RESULT 2
US-10-467-252-4
; Sequence 4, Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.
; APPLICANT: ARVIZU, Chandra S.; ELIOTT, Vicki S.;
; APPLICANT: HAFILIA, April J.A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y.Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dyang Aina M.;
; APPLICANT: GRAUB, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Rodrick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFPIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junling;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10467,252
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 90012430CD1
US-10-467-252-4

Query Match 99.8%; Score 1634; DB 16; Length 313;
Best Local Similarity 99.7%; Pred. No. 2,5e-134;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMGHNTSNSSCDPIVTPHLSLVYIVLIGLVGISILFLVKNKTRTSVTT 60
Db 1 MOKCDPSPMGHNTSNSSCDPIVTPHLSLVYIVLIGLVGISILFLVKNKTRTSVTT 60
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QY 61 MAVINLVVHVSFLLTVPEPRLTYLIKTTMFGLPCKEVSAMLIHMYLTFLFYVILVT 120
Db 61 MAVINLVVHVSFLLTVPEPRLTYLIKTTMFGLPCKEVSAMLIHMYLTFLFYVILVT 120
QY 121 RYLIFPKCKDKVEFYRKLHAVAASAGMMTLVIVVPLVVSRYGJHEEYNEHCXFKHKE 180
Db 121 RYLIFPKCKDKVEFYRKLHAVAASAGMMTLVIVVPLVVSRYGJHEEYNEHCXFKHKE 180
QY 181 LATVYKTIINMIVIVFAVAIVLLVPOVEITMLMVKLRSHLSHOEFMAQLKXLPFLIG 240
Db 181 LATVYKTIINMIVIVFAVAIVLLVPOVEITMLMVKLRSHLSHOEFMAQLKXLPFLIG 240
QY 241 VILVCELPYQPFRIYYLNVVTHSNACSSKVAFYNEIFLSTVAISCYDLLFPVGGSHWPK 300
Db 241 VILVCELPYQPFRIYYLNVVTHSNACSSKVAFYNEIFLSTVAISCYDLLFPVGGSHWPK 300
QY 301 OKIIGLMNCVLCR 313
Db 301 OKIIGLMNCVLCR 313

RESULT 3
US-09-782-974C-82
; Sequence 82, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogelii, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; FILE REFERENCE: 41USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-82

Query Match 98.4%; Score 1610; DB 10; Length 312;
Best Local Similarity 99.7%; Pred. No. 3.1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPPSPMGHNTSNSSCDPIVTPHLSLVYIVLIGLVGISILFLVKNKTRTSVTTMAVI 64
Db 4 DPPSPMGHNTSNSSCDPIVTPHLSLVYIVLIGLVGISILFLVKNKTRTSVTTMAVI 63
QY 65 NLVVHVSFLLTVPEPRLTYLIKTTMFGLPCKEVSAMLIHMYLTFLFYVILVTRYL 124
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DB 64 NLVVHVSFLITVPEFRITLYILIKTTWVGLEPFCKFVSAMLHIMVLTFLFVVLITVRYLI 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 303
QY 305 GLMNCVLCR 313
DB 304 GLMNCVLCR 312
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RESULT 4
US-10-467-492A-82
; Sequence 82, Application US/10467492A
; Publication No. US200506976A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: Novel G Protein Coupled Receptor
; FILE REFERENCE: 0411PHRM313
; CURRENT APPLICATION NUMBER: US/10/467,492A
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-492A-82
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Query Match 98.4%; Score 1610; DB 17; Length 312;
Best Local Similarity 99.7%; Pred. No. 3.1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DFPSPMGHNTSRNSCDPIVTPHILSLYFIYVILIGLVGVSILFLVKNKTRSVTTMAVI 64
DB 4 DFPSPMGHNTSRNSCDPIVTPHILSLYFIYVILIGLVGVSILFLVKNKTRSVTTMAVI 63
QY 65 NLVVHVSFLITVPEFRITLYILIKTTWVGLEPFCKFVSAMLHIMVLTFLFVVLITVRYLI 124
DB 64 NLVVHVSFLITVPEFRITLYILIKTTWVGLEPFCKFVSAMLHIMVLTFLFVVLITVRYLI 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 303
QY 305 GLMNCVLCR 313
DB 304 GLMNCVLCR 312
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RESULT 5  
US-10-975-979-82

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; Sequence 82, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Scheinin, Kathleen
; APPLICANT: Bannigan, Chris
; APPLICANT: Ruff, Valerie
; APPLICANT: Kayes, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Parodi, Luis
; APPLICANT: Hiesch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PHRM293
; CURRENT APPLICATION NUMBER: US/10/975,979
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-979-82
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Query Match 98.4%; Score 1610; DB 17; Length 312;
Best Local Similarity 99.7%; Pred. No. 3.1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DFPSPMGHNTSRNSCDPIVTPHILSLYFIYVILIGLVGVSILFLVKNKTRSVTTMAVI 64
DB 4 DFPSPMGHNTSRNSCDPIVTPHILSLYFIYVILIGLVGVSILFLVKNKTRSVTTMAVI 63
QY 65 NLVVHVSFLITVPEFRITLYILIKTTWVGLEPFCKFVSAMLHIMVLTFLFVVLITVRYLI 124
DB 64 NLVVHVSFLITVPEFRITLYILIKTTWVGLEPFCKFVSAMLHIMVLTFLFVVLITVRYLI 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHEKELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVEITIMLVOKLRHSLSHOFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFGSGHWFKOKII 303
QY 305 GLMNCVLCR 313
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Db 304 GLWNCVLGR 312

RESULT 6  
US-10-467-252-6

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Query Match	98.4%	Score 1610;	DB 16;	Length 367;
Best Local Similarity	99.7%	Pred. No. 3.7e-132;		
Matches 308; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

Qy	5	DPSMGNHTNSNSDCDPIVTEPHLSIXFPIYVIGGLNVAVISILFLVXKONRSTYMAVI	64
	59	DPSMGNHTNSNSDCDPIVTEPHLSIXFPIYVIGGLNVAVISILFLVXKONRSTYMAVI	118
Qy	65	NLVVHVSVELLVYFPRFLTYLTKTMMFGPFCFKPSAMATHIMYTLFLEYVILVYTYLI	124
Db	119	NLVVHVSVELLVYFPRFLTYLTKTMMFGPFCFKPSAMATHIMYTLFLEYVILVYTYLI	178
Qy	125	FFCKCKQVEFYRKLNAAVASAGMNTLVIVVPLVSVSYGIHEEYNEBCEKFKELAYT	184
Db	179	FFCKCKQVEFYRKLNAAVASAGMNTLVIVVPLVSVSYGIHEEYNEBCEKFKELAYT	238
Qy	185	YXKINIMYVIVIVANAVILLVPOYFIMLMYQKLRHLSHOFMAQKMLFPIGYILV	244
	239	YXKINIMYVIVIVANAVILLVPOYFIMLMYQKLRHLSHOFMAQKMLFPIGYILV	298

QY	QY	QY	QY
245	CFPLPYQPFPIYYLYLVVYTHSNACSSKVAARYNELPLSVYALISCYDILLPLVPGSHHFKOKII	304	
299	CFPLPYQPFPIYYLYLVVYTHSNACSKVAARYNELPLSVYALISCYDILLPLVPGSHHFKOKII	358	
305	GLMNCYLVCR 313		
359	GLMNCYLVCR 367		

RESULT 7  
US-10-292-798-1008  
; Sequence 1008, Application US/10292798  
; Publication No. US2003023583A1  
; GENERAL INFORMATION:

APPLICANT: ASAI, KIYOSHI  
 APPLICANT: AKIYAMA, YUTAKA  
 APPLICANT: ABEURATANI, HIROYUKI  
 TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
 FILE REFERENCE: 084355/166  
 CURRENT APPLICATION NUMBER: US/10/292,798  
 CURRENT FILING DATE: 2002-11-13  
 PRIOR APPLICATION NUMBER: 10/017,161  
 PRIOR FILING DATE: 2001-12-18  
 PRIOR APPLICATION NUMBER: JP 2001-246789  
 PRIOR FILING DATE: 2001-06-18  
 NUMBER OF SEQ. ID NOS: 2070  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ. ID NO: 1008  
 LENGTH: 448  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-292-798-1008

Query Match	98.4%	Score 1610;	DB 15;	Length 448;
Best Local Similarity	99.7%	Pred. No. 4.6e-132;		
Matches 308; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

Qy	5	DPSMNGHTSNSSCDPLVPHLISLVEIYLIGLGVGISLEFLKNNTRSYTMAYV	64
Dp	4	DPSMNGHTSNSSCDPLVPHLISLVEIYLIGLGVGISLEFLKNNTRSYTMAYV	63
Qy	65	NLVVHVSFLTLVPRLTYLLIKTMMFGLPFCFVSAMLHIMVLYFLFYVLLVTRYLL	124
Dp	64	NLVVHVSFLTLVPRLTYLLIKTMMFGLPFCFVSAMLHIMVLYFLFYVLLVTRYLL	123
Qy	125	FPFCCKQKVEFYKFLANVAASAGMMTLVIVIVPLVVSRYGHEEYNEHCQFKHKELAYT	184
Dp	124	FPFCCKQKVEFYKFLANVAASAGMMTLVIVIVPLVVSRYGHEEYNEHCQFKHKELAYT	183
Qy	185	YVKIINMVLIVFVIAVAIILLVFOVFIIIMLVOKLRHSLSHOEPMALKNLFFIGVILV	244
Dp	184	YVKIINMVLIVFVIAVAIILLVFOVFIIIMLVOKLRHSLSHOEPMALKNLFFIGVILV	243
Qy	245	CFPLPYQFPIIYLYLVNTVTSNACSSVAFVYNEIFLSVTAISCYDILLFPVGGSHMPKOKII	304
Dp	244	CFPLPYQFPIIYLYLVNTVTSNACSSVAFVYNEIFLSVTAISCYDILLFPVGGSHMPKOKII	303
Qy	305	GLMNCVLCR 313	
Dp	304	GLMNCVLCR 312	

RESULT 8  
US-09-995-225-4  
; Sequence 4, Application US/09995225  
; Publication No. US20020193584A1

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; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.

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APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human C
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
PRIORITY FILING DATE: 2001-11-26
PRIORITY FILING DATE: 1998-10-13
PRIORITY FILING DATE: PCT/US99/23938
PRIORITY FILING DATE: 1998-10-13
PRIORITY FILING DATE: 60/253,404
PRIORITY FILING DATE: 2000-11-27
PRIORITY FILING DATE: 60/255,366
PRIORITY FILING DATE: 2000-12-12
PRIORITY FILING DATE: 60/270,286
PRIORITY FILING DATE: 2001-02-20
PRIORITY FILING DATE: 60/282,365
PRIORITY FILING DATE: 2001-04-06
PRIORITY FILING DATE: 60/270,266
PRIORITY FILING DATE: 2001-02-20
PRIORITY FILING DATE: 60/282,032
PRIORITY FILING DATE: 2001-04-06
PRIORITY FILING DATE: 60/282,358
PRIORITY FILING DATE: 2001-04-06
PRIORITY FILING DATE: 60/282,356
PRIORITY FILING DATE: 2001-04-06
PRIORITY FILING DATE: 2001-05-14
PRIORITY FILING DATE: 60/309,208
PRIORITY FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-225-4
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DB 61 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 120
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DB 121 KQKVEFYRKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCPEKHELAITYYVKI 180
QY 189 INMYIVIFVAIVAVILLVPOVFTIMLMVQKLRHSLSHQEFMAQKNLFFIGVILVCFPL 248
DB 181 INMYIVIFVAIVAVILLVPOVFTIMLMVQKLRHSLSHQEFMAQKNLFFIGVILVCFPL 240
QY 249 YQFFRIYYLNVVTHSNACSKVAFYNEIFLSTVAISCYDILLFVGGSHWFKOKIIGLWN 308
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; Sequence 4, Application US/09995225
; Publication No. US2003019588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
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APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Hong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US2003019588A9-Endogenous Versions of Human
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
PRIORITY FILING DATE: 2001-11-26
PRIORITY FILING DATE: 1998-10-13
PRIORITY FILING DATE: PCT/US99/23938
PRIORITY FILING DATE: 1998-10-13
PRIORITY FILING DATE: 60/253,404
PRIORITY FILING DATE: 2000-11-27
PRIORITY FILING DATE: 60/255,366
PRIORITY FILING DATE: 2000-12-12
PRIORITY FILING DATE: 60/270,286
PRIORITY FILING DATE: 2001-02-20
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PRIORITY FILING DATE: 60/282,358
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PRIORITY FILING DATE: 60/282,356
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PRIORITY FILING DATE: 2001-05-14
PRIORITY FILING DATE: 60/309,208
PRIORITY FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-225-4
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Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 61 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 120
QY 129 KQKVEFYRKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCPEKHELAITYYVKI 188
DB 121 KQKVEFYRKLAHVAASAGMTLVIVVPLVVSRYGHEEYNEHCPEKHELAITYYVKI 180
QY 189 INMYIVIFVAIVAVILLVPOVFTIMLMVQKLRHSLSHQEFMAQKNLFFIGVILVCFPL 248
DB 181 INMYIVIFVAIVAVILLVPOVFTIMLMVQKLRHSLSHQEFMAQKNLFFIGVILVCFPL 240
QY 249 YQFFRIYYLNVVTHSNACSKVAFYNEIFLSTVAISCYDILLFVGGSHWFKOKIIGLWN 308
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QY 309 CVLCR 313
DB 301 CVLCR 305
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US-10-055-106C-2
; Sequence 2, Application US/10055106C
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/ Publication No. US20030017536A1
/ GENERAL INFORMATION:
/ APPLICANT: Pfizer Inc.
/ TITLE OF INVENTION: Novel Polypeptide
/ FILE REFERENCE: PC10970AGLK
/ CURRENT APPLICATION NUMBER: US/10/055,106C
/ CURRENT FILING DATE: 2002-01-23
/ PRIOR APPLICATION NUMBER: GB0101739.1
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: US 60/267,341
/ PRIOR FILING DATE: 2001-02-08
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-055-106C-2
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DB 61 VHSVFLTVPRFLTYLIKTTMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 180
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 248
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 240
QY 249 YQFFRIYYLVNVTTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKIIGLMN 308
DB 241 YQFFRIYYLVNVTTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKIIGLMN 300
QY 309 CYLCKR 313
DB 301 CYLCKR 305
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US-10-188-405-10
/ Sequence 10, Application US/10188405
/ Publication No. US20030082585A1
/ GENERAL INFORMATION:
/ APPLICANT: Tian, Hui
/ APPLICANT: Dai, Kang
/ APPLICANT: Chen, Jin-Long
/ APPLICANT: Zhao, Jia-gang
/ APPLICANT: Cui, Gene
/ APPLICANT: Tularik Inc.
/ TITLE OF INVENTION: No. US20030082585A1e1 Receptors
/ FILE REFERENCE: 018781-008410US
/ CURRENT APPLICATION NUMBER: US/10/188,405
/ CURRENT FILING DATE: 2002-07-01
/ PRIOR APPLICATION NUMBER: US 60/302,800
/ PRIOR FILING DATE: 2001-07-03
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
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/ OTHER INFORMATION: human TGR343
US-10-188-405-10
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Query Match          96.9%; Score 1587; DB 14; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGHNTSRNSCDPIVTPHLISLYFIYLIGLVGISILFLVKNTRSVTTMAVINLV 60
QY 69 VHSVFLTVPRFLTYLIKTTMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 128
DB 61 VHSVFLTVPRFLTYLIKTTMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 180
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 248
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 240
QY 249 YQFFRIYYLVNVTTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKIIGLMN 308
DB 241 YQFFRIYYLVNVTTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKIIGLMN 300
QY 309 CYLCKR 313
DB 301 CYLCKR 305
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/ Sequence 2, Application US/10293171
/ Publication No. US20030138418A1
/ GENERAL INFORMATION:
/ APPLICANT: Bishngdrelo, Hafeng
/ APPLICANT: Cai, Jidong
/ APPLICANT: Gassenhuber, Johann
/ TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH
/ FILE REFERENCE: USAV2001/0158 US NP
/ CURRENT APPLICATION NUMBER: US/10/293,171
/ CURRENT FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: US60/354,150
/ PRIOR FILING DATE: 2001-11-13
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-293-171-2
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Query Match          96.9%; Score 1587; DB 14; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGHNTSRNSCDPIVTPHLISLYFIYLIGLVGISILFLVKNTRSVTTMAVINLV 60
QY 69 VHSVFLTVPRFLTYLIKTTMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 128
DB 61 VHSVFLTVPRFLTYLIKTTMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYYKI 180
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 248
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHOEFWAOLKNLFFIGVILVCFLP 240
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Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
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Qy	69	VHSVFLITVPFRLTYLIKKTMMGLPFCKFVSAMLIHMYLTPLFYVILVTRYLIFPKC	128
Db	61	VHSVFLITVPFRLTYLIKKTMMGLPFCKFVSAMLIHMYLTPLFYVILVTRYLIFPKC	120
Qy	129	KDKVEFYRDLAAVASAGMTLVIIVVBLVVSRYGHEEYNEBEHCFKHELATYYKI	188
Db	121	KDKVEFYRDLAAVASAGMTLVIIVVBLVVSRYGHEEYNEBEHCFKHELATYYKI	180
Qy	189	INMYIVIFVIAVAAILLVQVFIIMLMVQKLHSHLSHOEFMAOLKNLFFIGVILVCFLP	248
Db	181	INMYIVIFVIAVAAILLVQVFIIMLMVQKLHSHLSHOEFMAOLKNLFFIGVILVCFLP	240
Qy	249	YQFFRIYYLNVVTHSNACSSKVAFNEIFLSTYAI SCYDILLFVFGGSHWFKOKIIGLMN	308
Db	241	YQFFRIYYLNVVTHSNACNSKVAFNEIFLSTYAI SCYDILLFVFGGSHWFKOKIIGLMN	300
Qy	309	CVLCR 313	
Db	301	CVLCR 305	

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 Job time : 76 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:50:20 / Search time 4221.38 Seconds

(without alignments)  
10778.327 Million cell updates/sec

Title: US-10-085-233B-3

Perfect score: 939  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: 1: gb ba: \*  
2: gb hlg: \*  
3: gb in: \*  
4: gb om: \*  
5: gb ov: \*  
6: gb pat: \*  
7: gb ph: \*  
8: gb pl: \*  
9: gb pr: \*  
10: gb ro: \*  
11: gb sts: \*  
12: gb sy: \*  
13: gb un: \*  
14: gb vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	937.4	99.8	1336	6	AX709193 Sequence
2	928.2	98.8	1340	6	AX709194 Sequence
3	928.2	98.8	1460	6	AX709195 Sequence
4	928.2	98.8	2525	6	AX147836 Sequence
5	928.2	98.8	2525	6	AX521885 Sequence
6	927.8	98.8	113306	6	AX646815 Sequence
7	927.8	98.8	218186	9	AC083865 Homo sapi
8	927.8	98.8	1332	6	CQ737895 Sequence
9	926.2	98.6	1051	6	AX453412 Sequence
10	923	98.3	162268	9	AC146385 Pan trogl
11	913.4	97.3	918	6	BD187510 Novel Pol
12	913.4	97.3	918	6	AX481576 Sequence
13	913.4	97.3	918	6	AX498180 Sequence
14	913.4	97.3	918	6	BD105324 Sequence
15	913.4	97.3	918	9	AY288420 Homo sapi
16	907.4	96.6	1499	6	AX451925 Sequence
17	690	73.5	972	6	AX651538 Sequence
18	635	67.6	206999	10	AC122886 Mus muscu
19	633.4	67.5	167316	2	AC078995 Mus muscu

20	631.8	67.3	918	10	AY288427 Mus muscu
21	524.4	55.8	228766	2	AC099132 Rattus no
22	456	48.6	4456	9	AY255538 Homo sapi
23	451.6	48.1	140539	2	AC079758 Homo sapi
24	433	46.1	744	10	AY288432 Rattus no
25	404.4	43.1	447	6	AX147776 Sequence
26	404.4	43.1	447	6	AX521825 Sequence
27	275.2	29.3	393	10	AY255553 Mus muscu
28	184	19.6	169155	5	BX088685 Zebrafish
29	184	19.6	173882	5	BX640462 Zebrafish
30	144.8	15.4	897	6	BD182016 Novel G p
31	103.4	11.0	140539	2	AC079758 Homo sapi
32	103.4	11.0	225912	2	AC084210 Homo sapi
33	76.4	8.1	1113	6	AX280917 Sequence
34	76.4	8.1	1113	9	AY268428 Homo sapi
35	76.4	8.1	1113	9	CR542082 Homo sapi
36	76.4	8.1	1252	9	HUMOPRLP L40949 Homo sapi
37	76.4	8.1	1379	9	AF348323 Homo sapi
38	76.4	8.1	1805	6	AX746239 Sequence
39	76.4	8.1	1973	6	AR270828 Sequence
40	76.4	8.1	1973	6	AR380872 Sequence
41	76.4	8.1	1973	9	HSORL1 X77130 H. sapiens m
42	76.4	8.1	2534	6	AX548923 Sequence
43	76.4	8.1	2534	9	HSU30185 Human orpha
44	76.4	8.1	3205	6	AR447599 Sequence
45	76.4	8.1	3420	9	BC038433 Homo sapi

#### ALIGNMENTS

RESULT 1	AX709193	Sequence 52 from Patent WO02063004.	1336 bp	DNA	linear	PAT 04-APR-2003
LOCUS	AX709193					
DEFINITION	AX709193					
ACCESSION	AX709193					
VERSION	AX709193.1	GI:29564787				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE						
AUTHORS	Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallik, D.A., Ganchi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S., Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R., Burford, N., Lu, D.A., Grail, R.C., Khan, F.A., Walsh, R.T., Ison, C.H., Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.					
TITLE	G-protein coupled receptors					
JOURNAL	Patent: WO 02063004-A 52 15-AUG-2002;					
FEATURES	Incyte Genomics, Inc. (US)					
source	1. 1336					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
	/note="Incyte ID No: 90012430CB1"					
ORIGIN						
Query Match	99.8%; Score 937.4; DB 6; Length 1336;					
Best Local Similarity	99.9%; Pred. No. 2.8e-235;					
Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
OY	1 ATGCAAAATGATGCTTCCCAAGTATGCTGGGCAATACCTCCGAGATTCCTTGC 60					
Db	195 ATGCAAAATGATGCTTCCCAAGTATGCTGGGCAATACCTCCGAGATTCCTTGC 254					
OY	61 GATCTTATAGTGAACCCCACTTAATACGCTCTTACTTATAGTGTATTTGGCGGCTG 120					
Db	255 GATCTTATAGTGAACCCCACTTAATACGCTCTTACTTATAGTGTATTTGGCGGCTG 314					
OY	121 GTGGGTGTCATTTCCCTTTTCTCTGTTGAATAAACCAGGCTGACGACACC 180					

|||||  
Db 315 GTGGGTGTCATTTCCATTTCTTTCCCTCGTGTAATAATGACACCCGGTCAAGTACAC 374  
|||  
Qy 181 ATGGCGGTGATTAATTTGGTGGTGTCCACAGCGTTTTCGTGTGACAGTCCATTGCG 240  
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Db 375 ATGGCGGTGATTAATTTGGTGGTGTCCACAGCGTTTTCGTGTGACAGTCCATTGCG 434  
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Qy 241 TTGAGCTGCTGATTCAGAAAGACTTGAGATGTTGGGCTGCCCTTGCAAAATTTGAGT 300  
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Db 435 TTGAGCTGCTGATTCAGAAAGACTTGAGATGTTGGGCTGCCCTTGCAAAATTTGAGT 494  
|||  
Qy 301 GCCATGCTGCACATCCACATGTAACCTCAAGTTCCTATTCTATGTTGATGATCCGTAC 360  
|||  
Db 495 GCCATGCTGCACATCCACATGTAACCTCAAGTTCCTATTCTATGTTGATGATCCGTAC 554  
|||  
Qy 361 AGATACCTGATCTTTCTTCAAGTGCAAGAATAAGTGAATTTCTACAGAAATGTCATGCT 420  
|||  
Db 555 AGATACCTGATCTTTCTTCAAGTGCAAGAATAAGTGAATTTCTACAGAAATGTCATGCT 614  
|||  
Qy 421 GTGGCTGCCAGTGTGGCATGTGGAGAGCTGTGATGTCATGTGGTACCCCTGTGTGTC 480  
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Db 615 GTGGCTGCCAGTGTGGCATGTGGAGAGCTGTGATGTCATGTGGTACCCCTGTGTGTC 674  
|||  
Qy 481 TCCCGGTATGGAATCCATGAGGAATCAATAGAGACACGTGTTTAAATTTCAAAAGAG 540  
|||  
Db 675 TCCCGGTATGGAATCCATGAGGAATCAATAGAGACACGTGTTTAAATTTCAAAAGAG 734  
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Qy 541 CTTCGTTTACACATATGTGAATAATCATATATATATATATATATATATATATATATAT 600  
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Db 735 CTTCGTTTACACATATGTGAATAATCATATATATATATATATATATATATATATATAT 794  
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Qy 601 GCGTGATCTGTGTGCTTCCAGGTCTTCATCATATATATATATATATATATATATATAT 660  
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Db 795 GCGTGATCTGTGTGCTTCCAGGTCTTCATCATATATATATATATATATATATATATAT 854  
|||  
Qy 661 CACTCTTCTACTATCCACACAGAGAGTCTGGGCTCAAGTCAAAACCTATTTTATATAG 720  
|||  
Db 855 CACTCTTCTACTATCCACACAGAGAGTCTGGGCTCAAGTCAAAACCTATTTTATATAG 914  
|||  
Qy 721 GTCATCTTGTGTTGTTCTTCCCTACAGTCTTTAGATCTATATATATATATATATATAT 780  
|||  
Db 915 GTCATCTTGTGTTGTTCTTCCCTACAGTCTTTAGATCTATATATATATATATATATAT 974  
|||  
Qy 781 AGCATTTTCAATGCTGTGAGACAGAGTGTGATTTTATATATATATATATATATATATAT 840  
|||  
Db 975 AGCATTTTCAATGCTGTGAGACAGAGTGTGATTTTATATATATATATATATATATAT 1034  
|||  
Qy 841 ACAGCAATTAGCTGTATGATTTGCTTCTTGTCTTTGGGGGAAGCCATTGGTTAAG 900  
|||  
Db 1035 ACAGCAATTAGCTGTATGATTTGCTTCTTGTCTTTGGGGGAAGCCATTGGTTAAG 1094  
|||  
Qy 901 CAAAAGATATTTGGCTTATGAAATGTGTTTGTGCCGT 939  
|||  
Db 1095 CAAAAGATATTTGGCTTATGAAATGTGTTTGTGCCGT 1133  
|||  
RESULT 2  
AX709194 1340 bp DNA linear PAT 04-APR-2003  
LOCUS Sequence 53 from Patent WO02063004.  
DEFINITION AX709194  
ACCESSION AX709194  
VERSION AX709194.1 GI:29564788  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS  
Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,  
Hafalik, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,  
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and

|||||  
Qy 7 AATGTGACTTCCCAAGATATGCTGGCCACATACCTCCAGGAATTCCTTGGATCCT 66  
|||  
Db 205 ACAGGTGACTTCCCAAGATATGCTGGCCACATACCTCCAGGAATTCCTTGGATCCT 264  
|||  
Qy 67 ATAGTACACCCCACTTATATGAGCTTACTTACTTATGAGCTTATGAGGAGGCTGGTGGT 126  
|||  
Db 265 ATAGTACACCCCACTTATATGAGCTTACTTACTTATGAGCTTATGAGGAGGCTGGTGGT 324  
|||  
Qy 127 GTCAATTCATCTTTTCTCTCGGTGAAATGAAACACCCGGTCAAGTCAAGTCAAGTCA 186  
|||  
Db 325 GTCAATTCATCTTTTCTCTCGGTGAAATGAAACACCCGGTCAAGTCAAGTCAAGTCA 384  
|||  
Qy 187 GTCAATTCATCTTTTCTCTCGGTGAAATGAAACACCCGGTCAAGTCAAGTCAAGTCA 246  
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Db 385 GTCAATTCATCTTTTCTCTCGGTGAAATGAAACACCCGGTCAAGTCAAGTCAAGTCA 444  
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Qy 247 TACCTATCAAAAGACATTTGATTTGGGCTGCCCTCTGCAAAATTTGATGAGTGCATG 306  
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Db 445 TACCTATCAAAAGACATTTGATTTGGGCTGCCCTCTGCAAAATTTGATGAGTGCATG 504  
|||  
Qy 307 CTGACATGCAATGATCTTCAAGTCTTCTTCTATGATGATGATGATGATGATGATGATG 366  
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Db 505 CTGACATGCAATGATCTTCAAGTCTTCTTCTATGATGATGATGATGATGATGATGATG 564  
|||  
Qy 367 CTGATCTTCTTCAAGTGCAGAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCT 426  
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Db 565 CTGATCTTCTTCAAGTGCAGAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCT 624  
|||  
Qy 427 GCCAGTGTGATGATGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 486  
|||  
Db 625 GCCAGTGTGATGATGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 684  
|||  
Qy 487 TATGGAATCATGAGGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
|||  
Db 685 TATGGAATCATGAGGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 744  
|||  
Qy 547 TACACATATGTAATAATCATCAATATATATATATATATATATATATATATATATATAT 606  
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Db 745 TACACATATGTAATAATCATCAATATATATATATATATATATATATATATATATATAT 804  
|||  
Qy 607 ATTCTGTGTGCTTCTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 666  
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Db 805 ATTCTGTGTGCTTCTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 864  
|||  
Qy 667 TTACTATGCCACAGAGAGTCTGGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 726  
|||  
Db 865 TTACTATGCCACAGAGAGTCTGGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 924  
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Qy 727 CTTCGTTTGTTCCTTCCCTACAGTCTTTAGATCTATATATATATATATATATATATAT 786  
|||  
Db 925 CTTCGTTTGTTCCTTCCCTACAGTCTTTAGATCTATATATATATATATATATATATAT 984  
|||  
Qy 787 TCCATGCTGTGAGACAGAGTGTGATTTTATACGAATCTTCTTGAAGTGAACAGAG 846  
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Db 985 TCCATGCTGTGAGACAGAGTGTGATTTTATACGAATCTTCTTGAAGTGAACAGAG 1044  
|||  
Qy 847 ATTAGGTGAT 906  
|||

DB 1045 ATTAGCTGATGATTTGCTCTCTTTGGGGAGACCAATGGTTAAACAAAG 1104  
QY 907 ATATGGCTTATGGAATGCTTTTGGCCGT 939  
DB 1105 ATATGGCTTATGGAATGCTTTTGGCCGT 1137

RESULT 3  
AX709195 1460 bp DNA linear PAT 04-APR-2003  
LOCUS Sequence 54 from Patent WO02063004.  
DEFINITION AX709195  
ACCESSION AX709195  
VERSION AX709195.1 GI:29564789  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Baughn M.R., Tribouley C.M., Nguyen D.B., Thornton M., Yao M.G.,  
Kallick D.A., Gandhi A.R., Walla N.K., Arvizu C., Elliott V.S.,  
Hafalla A.J., Ramkumar J., Pei J., Tang Y.T., Yue H., Reddy R.,  
Burford N., Lu D.A., Grail R.C., Khan F.A., Walsh R.T., Ison C.H.,  
Richardson T.W., Griffin J.A., Warren B.A., Yang J., Lee E.A. and  
Harland L.  
G-protein coupled receptors  
Patent: WO 02063004-A 54.15-AUG-2002;  
Incyte Genomics, Inc. (US)  
Location/Qualifiers  
1. 1460  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 90012670CB1"

ORIGIN  
Query Match 98.8%; Score 928.2; DB 6; Length 1460;  
Best Local Similarity 99.7%; Pred. No. 7.5e-233;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAATGACTTCCCAAGATATGCTGACCAATACCTTCAGAAATCTCTGCAATCCT 66  
DB 325 AAGAGTACTTCCCAAGATATGCTGACCAATACCTTCAGAAATCTCTGCAATCCT 384  
QY 67 ATATGACACCCCACTTAATGAGCTTACTTCAATGAGCTTAATGAGCTTATGAGCT 126  
DB 385 ATATGACACCCCACTTAATGAGCTTACTTCAATGAGCTTATGAGCTTATGAGCT 444  
QY 127 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 186  
DB 445 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 504  
QY 187 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 246  
DB 505 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 564  
QY 247 TACCTGATCAAGAAAGATGATGTTGGCTGCCCTTTCGAAATTTGAGTGCATG 306  
DB 565 TACCTGATCAAGAAAGATGATGTTGGCTGCCCTTTCGAAATTTGAGTGCATG 624  
QY 307 CTGCAATCCCAATGATACCTGATGCTTCTTATGATGATGATGCTGATGATGATGATG 366  
DB 625 CTGCAATCCCAATGATACCTGATGCTTCTTATGATGATGATGCTGATGATGATGATG 684  
QY 367 CTGATCTTCTTCAAGTCAAGAAAGAAAGTGAATTTCTACAGAAATCTGATGAGCT 426  
DB 685 CTGATCTTCTTCAAGTCAAGAAAGAAAGTGAATTTCTACAGAAATCTGATGAGCT 744  
QY 427 GCCAGTGTGGATGTGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 486  
DB 745 GCCAGTGTGGATGTGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 804

QY 487 TATGAAATCCATGAGGAATAATGAGAGACCTGTTTAAATTCACAAAGCTTGT 546  
DB 805 TATGAAATCCATGAGGAATAATGAGAGACCTGTTTAAATTCACAAAGCTTGT 864  
QY 547 TACACATATGATGAAATATCAATCAATATGATGATGATGATGATGATGATGATGATG 606  
DB 865 TACACATATGATGAAATATCAATCAATATGATGATGATGATGATGATGATGATGATG 924  
QY 607 ATTCTGTGGTCTTCCAGGCTTCTCATCATATATGATGATGATGATGATGATGATGATG 666  
DB 925 ATTCTGTGGTCTTCCAGGCTTCTCATCATATATGATGATGATGATGATGATGATGATG 984  
QY 667 TTACTATCCCAACAGAGAGTCTGAGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 726  
DB 985 TTACTATCCCAACAGAGAGTCTGAGGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1044  
QY 727 CTGTTGTTGTTCTTCCCTCAACAGTCTTCTTGAAGATCTTCTTGAATGTTGATGATG 786  
DB 1045 CTGTTGTTGTTCTTCCCTCAACAGTCTTCTTGAAGATCTTCTTGAATGTTGATGATG 1104  
QY 787 TCCAAATGCTGTTGACGACCAAGTTCATTTATPAAGAAATCTTCTTGAATGTTGATG 846  
DB 1105 TCCAAATGCTGTTGACGACCAAGTTCATTTATPAAGAAATCTTCTTGAATGTTGATG 1164  
QY 847 ATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906  
DB 1165 ATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1224  
QY 907 ATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 939  
DB 1225 ATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257

RESULT 4  
AX147836 2525 bp DNA linear PAT 08-JUN-2001  
LOCUS Sequence 81 from Patent WO0136473.  
DEFINITION AX147836  
ACCESSION AX147836.1 GI:14346839  
VERSION AX147836.1  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Vogel J., Wood L.S., Parodi L.A., Hiesbach R.R., Lind P.,  
Slightom J., Schejlin K.A., Kayles P.S., Bannigan C.M., Ruff V.,  
Sejltz T. and Huff R.M.  
Novel g protein-coupled receptors  
Patent: WO 0136473-A 81.25-MAY-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
Location/Qualifiers  
1. 2525  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 98.8%; Score 928.2; DB 6; Length 2525;  
Best Local Similarity 99.7%; Pred. No. 8e-233;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAATGACTTCCCAAGATATGCTGACCAATACCTTCAGAAATCTCTGCAATCCT 66  
DB 9 AAGAGTACTTCCCAAGATATGCTGACCAATACCTTCAGAAATCTCTGCAATCCT 68  
QY 67 ATATGACACCCCACTTAATGAGCTTACTTCAATGAGCTTATGAGCTTATGAGCT 126  
DB 69 ATATGACACCCCACTTAATGAGCTTACTTCAATGAGCTTATGAGCTTATGAGCT 128  
QY 127 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 186  
DB 129 GTCATTTCCATTTCTTTCCCTCCGCGAATAATGAACCCCGTCAAGTACCAATGAGCT 188



Oy	187	GTCAATPAACTGGTGTGTGTGTCCACAGCGTTTTCCTGTGCACAGTGCATTTTGGCTTTGACC	246
Db	189	GTCAATPAACTGGTGTGTGTGTCCACAGCGTTTTCCTGTGCACAGTGCATTTTGGCTTTGACC	248
Oy	247	TACCTCATCAAGAAGACTTGGATGTTTGGGCTGGCCCTTCTGCAAAATTTGTGAGTGCATG	306
Db	249	TACCTCATCAAGAAGACTTGGATGTTTGGGCTGGCCCTTCTGCAAAATTTGTGAGTGCATG	308
Oy	307	CTGCACATCCACATGTATCTCAGCTTCTCTATTCTATGTGTGTATCTTGTGTACCCAGATATC	366
Db	309	CTGCACATCCACATGTATCTCAGCTTCTCTATTCTATGTGTGTATCTTGTGTATCCAGATATC	368
Oy	367	CTCAATCTCTTCAAGTGTGAAGACAAAGTGGAAATTTCTACAGAAAACCTGCATGCTGGGCT	426
Db	369	CTCAATCTCTTCAAGTGTGAAGACAAAGTGGAAATTTCTACAGAAAACCTGCATGCTGGGCT	428
Oy	427	GCCAGTGTGTGCATGTGTGACCGCTGTGTGATTTGTCAATGTGTGTACCCCTGTGTGTCTCCGG	486
Db	429	GCCAGTGTGTGCATGTGTGACCGCTGTGTGATTTGTCAATGTGTGTATCCCTGTGTGTCTCCGG	488
Oy	487	TATGGAATCCATGAGGAATACATGAGAGACACTGTTTTAAATTTTCACAAAAGACTTGTCT	546
Db	489	TATGGAATCCATGAGGAATACATGAGAGACACTGTTTTAAATTTTCACAAAAGACTTGTCT	548
Oy	547	TACACATATGTGAAGAAATCATCATATATATGATATGATTTTGTCTATAGCCGTGTGTGTG	606
Db	549	TACACATATGTGAAGAAATCATCATATATATGATATGATTTTGTCTATAGCCGTGTGTGTG	608
Oy	607	ATTGCTGTGTGCTTCTCCAGTCTTTCATCATATATATGATGTGTGACAAAGCTATGCGCACTCT	666
Db	609	ATTGCTGTGTGCTTCTCCAGTCTTTCATCATATATATGATGTGTGACAAAGCTATGCGCACTCT	668
Oy	667	TTACTATCCACACAGGAAGTTCTGGGCTCAAGCTGAAAAACCTATTTTTTTATATAGGGGTCAATC	726
Db	669	TTACTATCCACACAGGAAGTTCTGGGCTCAAGCTGAAAAACCTATTTTTTTATATAGGGGTCAATC	728
Oy	727	CTGTGTTGTTCCTCTCCCTACACAGTCTTTAGAGATCATATCACTTGAATGTGTGACGCAT	786
Db	729	CTGTGTTGTTCCTCTCCCTACACAGTCTTTAGAGATCATATCACTTGAATGTGTGACGCAT	788
Oy	787	TCCAAATGCTGTAGACGACGAAGTTTGATTTATACGAATCTTCTTGAGTGTAAACGACA	846
Db	789	TCCAAATGCTGTAGACGACGAAGTTTGATTTATACGAATCTTCTTGAGTGTAAACGACA	848
Oy	847	ATTAGCTGTATNGATTTGCTTCTCTTTGTCTTTTGGGGGAACCATTTGTTTATACCAAAAG	906
Db	849	ATTAGCTGTATNGATTTGCTTCTCTTTGTCTTTTGGGGGAACCATTTGTTTATACCAAAAG	908
Oy	907	ATTAATTTGGCTATAGGAATTGTGTTTGTGGCCGT	939
Db	909	ATTAATTTGGCTATAGGAATTGTGTTTGTGGCCGT	941
RESULT 5			
LOCUS	AX521885	2525 bp	DNA linear PAT 24-OCT-2002
DEFINITION	Sequence 81 from Patent WO02064789.		
ACCESSION	AX521885		
VERSION	AX521885.1	GI:24410791	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1	Lind, P., Parodi, L.A., Vogeli, G. and Wood, L.S.	
TITLE		G protein-coupled receptor	
JOURNAL		Patent: WO 02064789-A 81 22 AUG-2002;	
PHARMACIA & UPJOHN COMPANY (US)			
FEATURES			
source		Location/Qualifiers	
	1..2525	/organism="Homo sapiens"	

ORIGIN	Query Match	Best Local Matches	Similarity	Score	DB	Length	2525;
930;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps
0							
0Y	7	AAATGTACTTCCCAATATGCTGCGCCACAATATCTTCAGAAATTCCTCTTGCAATCT	66				
Db	9	ACAGGTGCTTCCCAAGTATGCTGCGCCACAATATCTTCAGAAATTCCTCTTGCAATCT	68				
0Y	67	ATATGACACCCCACTTAATCAGCCTCTACTTCAATAGCTTAATGCGGCGCTGCTGGCT	126				
Db	69	ATATGACACCCCACTTAATCAGCCTCTACTTCAATAGCTTAATGCGGCGCTGCTGGCT	128				
0Y	127	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGCTCAGTACCAACATGCGC	186				
Db	129	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGCTCAGTACCAACATGCGC	188				
0Y	187	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGCTCAGTACCAACATGCGC	246				
Db	189	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGCTCAGTACCAACATGCGC	248				
0Y	247	TACCTCATCAAGAAAGCTTGATGTTTGGGCTGCGCTTCTGCAATTTTGTAGTCCATG	306				
Db	249	TACCTCATCAAGAAAGCTTGATGTTTGGGCTGCGCTTCTGCAATTTTGTAGTCCATG	308				
0Y	307	CTGCAATATCCCAATATGATCTTCACTTCTTATATGATGATCTGCTCAGCAATAC	366				
Db	309	CTGCAATATCCCAATATGATCTTCACTTCTTATATGATGATCTGCTCAGCAATAC	368				
0Y	367	CTCATCTCTTCAAGTGCAGAAAGCAAAATGGAATTTCTACAGAAACTCATCTGCTGCT	426				
Db	369	CTCATCTCTTCAAGTGCAGAAAGCAAAATGGAATTTCTACAGAAACTCATCTGCTGCT	428				
0Y	427	GCCAGTGTGCAATGATGAGCGCTGCTGATGTCATTTGTGTACCCCTGCTGCTCCCG	486				
Db	429	GCCAGTGTGCAATGATGAGCGCTGCTGATGTCATTTGTGTACCCCTGCTGCTCCCG	488				
0Y	487	TATGAAATCCCAAGGAAATACAAAGAGAGACCTGTTTAAATTCACAAAGAGCTGCT	546				
Db	489	TATGAAATCCCAAGGAAATACAAAGAGAGACCTGTTTAAATTCACAAAGAGCTGCT	548				
0Y	547	TACACATATGGAATAATCATCACTATAATGATCATTTTGTGTCATAGCCGCTGCTG	606				
Db	549	TACACATATGGAATAATCATCACTATAATGATCATTTTGTGTCATAGCCGCTGCTG	608				
0Y	607	ATTCTGTGTGCTTCCAGGCTCTTCACTATATATGATGATGATGATGATGATGATGAT	666				
Db	609	ATTCTGTGTGCTTCCAGGCTCTTCACTATATATGATGATGATGATGATGATGATGAT	668				
0Y	667	TTACTATCCCAACAGAGATCTGCGGCTCAGCTGAAATACTATTTTATAGGGCTCATC	726				
Db	669	TTACTATCCCAACAGAGATCTGCGGCTCAGCTGAAATACTATTTTATAGGGCTCATC	728				
0Y	727	CTGTGTGTCTTCTCTCTTACCAAGTTCTTAAAGATCTATTAATCTGAAATGTTGTGACAT	786				
Db	729	CTGTGTGTCTTCTCTCTTACCAAGTTCTTAAAGATCTATTAATCTGAAATGTTGTGACAT	788				
0Y	787	TCCAAATGCTGTAAGAGAGAGGTCATTTTAAAGAAATCTTCTGATGATGATGATGATGAT	846				
Db	789	TCCAAATGCTGTAAGAGAGAGGTCATTTTAAAGAAATCTTCTGATGATGATGATGATGAT	848				
0Y	847	ATTAGCTGCTATGATTTGCTTCTCTTGTCTTCTTGGGGAGAGCCATGCTTAAAGCAAAAG	906				
Db	849	ATTAGCTGCTATGATTTGCTTCTCTTGTCTTCTTGGGGAGAGCCATGCTTAAAGCAAAAG	908				
0Y	907	ATTATTTGCTTATGAAATTTGTTTGTGCGCT	939				
Db	909	ATTATTTGCTTATGAAATTTGTTTGTGCGCT	941				

RESULT 6	AX646815	113306 bp	DNA	linear	PAT 04-MAR-2003
LOCUS	Sequence 1007 from Patent EP1270724.				
DEFINITION	AX646815				
ACCESSION	AX646815.1	GI:28799225			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.				
AUTHORS	Guanosine triphosphate-binding protein coupled receptors				
TITLE	Patent: EP 1270724-A, 1007 02-JAN-2003;				
JOURNAL	National Institute of Advanced Industrial Science and Technology (JP) ; Center for Advanced Science and Technology Incubation, Ltd. (JP)				
FEATURES	Location/Qualifiers				
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	/db_xref="GI:28799226"				
	/translation="MTGDPSPMPGHNTRNSCDPIVTPHLISLYFLVILGLVGVIS				
	ILFLVKNMTRSTYMAVILVNVSHVFLTPERLTYLIKMTGGLPKFVSAML				
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	RGIHNEHYNEHFKFKELATYYVKIINMVIYFLAAVILVQVIFIMLVQKL				
	RHSLSHOEFWAQLKNLFTGLVLCFLPYQFRIYLVNVTHSNCSNKAFAVNEIF				
	LSVTAISCYDLFLFVGSGSHMFKQKIGLMNCVLCRNSPGLTPCFSLILFLPLAM				
	ASGVHCSVLRIGEVREKCFPLRHRTDILCLMPFNHHTYAVVERSVYKLECSGTI				
	SAHCTLYLPDSSNSPASASQVAGITGHHNAQLIFVIVETGHHVHGQGLDLTTS"				
ORIGIN					
Query Match	98.8%; Score 927.8; DB 6; Length 113306;				
Best Local Similarity	99.8%; Pred. No. 1.6e-232;				
Matches 929; Conservative	0; Mismatches 2; Indels 0; Gaps 0;				
QY	9	ATGTGACTCCCAAGATAGCTGGCCACATACCTCCAGAAATTCCTTGGCATCTTAT	68		
DB	11524	AGGTGACTCCCAAGATAGCTGGCCACATACCTCCAGAAATTCCTTGGCATCTTAT	11583		
QY	69	AGTGACACCCCACTTATACGCTTACTCATAGTCTTATTTGGCGGGCTGGTGGGTGT	128		
DB	11584	AGTGACACCCCACTTATACGCTTACTCATAGTCTTATTTGGCGGGCTGGTGGGTGT	11643		
QY	129	CATTTCATTCTTTCTCTCTGTGTGAATGAACACCGGTCAGTGAACCAATGGCGGT	188		
DB	11644	CATTTCATTCTTTCTCTCTGTGTGAATGAACACCGGTCAGTGAACCAATGGCGGT	11703		
QY	189	CATTATCTGT	248		
DB	11704	CATTATCTGT	11763		
QY	249	CCTCATCAAGAAAGACTTGATGTTGGGCTGACCTTCGTGAATTTGTGTGAGCCATGCT	308		
DB	11764	CCTCATCAAGAAAGACTTGATGTTGGGCTGACCTTCGTGAATTTGTGTGAGCCATGCT	11823		
QY	309	GCAATCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	368		
DB	11824	GCAATCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11883		
QY	369	CATCTTCTTCAAGTGCAAGACAAAGTGAATTTACAGAAAATCTGATGCTGTGCTGC	428		
DB	11884	CATCTTCTTCAAGTGCAAGACAAAGTGAATTTACAGAAAATCTGATGCTGTGCTGC	11943		
QY	429	CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	488		
DB	11944	CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	12003		
QY	489	TGGAATTCATGAGAAATACATAGAGACACTGTTTAAATTTACAAAAGCTTGCTTA	548		
DB	12004	TGGAATTCATGAGAAATACATAGAGACACTGTTTAAATTTACAAAAGCTTGCTTA	12063		
QY	549	CACATATGGAAGAAATATCAATCATATGATGATGATGATGATGATGATGATGATGAT	608		
DB	12064	CACATATGGAAGAAATATCAATCATATGATGATGATGATGATGATGATGATGATGAT	12123		
QY	609	TCTGTGTCTTCCAGATCTTCAATCATATGATGATGATGATGATGATGATGATGATGAT	668		
DB	12124	TCTGTGTCTTCCAGATCTTCAATCATATGATGATGATGATGATGATGATGATGATGAT	12183		
QY	669	ACTATCCACAGAGAGTGTGGGCTCACTGAAAAACCTATTTTATAGGGGTCAATCCT	728		
DB	12184	ACTATCCACAGAGAGTGTGGGCTCACTGAAAAACCTATTTTATAGGGGTCAATCCT	12243		
QY	729	TGTTGTCTTCCCTCCACAGTCTTTAGATCTATTAATGATGATGATGATGATGATGATGAT	788		
DB	12244	TGTTGTCTTCCCTCCACAGTCTTTAGATCTATTAATGATGATGATGATGATGATGATGAT	12303		
QY	789	CAATGCTGTAGCAGCAGAGTTCATTTTATACGAATCTTCTGATGATGATGATGATGAT	848		
DB	12304	CAATGCTGTAGCAGCAGAGTTCATTTTATACGAATCTTCTGATGATGATGATGATGAT	12363		
QY	849	TAGCTGCTATGATTTGCTTCTTGTCTTTGGGGGAAGCATTTGTTAAGCAAAAGAT	908		
DB	12364	TAGCTGCTATGATTTGCTTCTTGTCTTTGGGGGAAGCATTTGTTAAGCAAAAGAT	12423		
QY	909	AATTTGCTTATGGAATTTGTTGGCCGT	939		
DB	12424	AATTTGCTTATGGAATTTGTTGGCCGT	12454		
RESULT 7	AC083865	218186 bp	DNA	linear	PRI 26-JAN-2001
LOCUS	Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.				
DEFINITION	AC083865				
ACCESSION	AC083865.2	GI:12545315			
VERSION					
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.				
AUTHORS	Large-scale Mapping and Sequencing of Human Chromosome 7				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 218186)				
REFERENCE	Kaul, R., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (04-OCT-2000) Genome Center, University of Washington,				
TITLE	Box 352145, Seattle, WA 98195, USA				
AUTHORS	3 (bases 1 to 218186)				
REFERENCE	Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (26-JAN-2001) Genome Center, University of Washington,				
TITLE	Box 352145, Seattle, WA 98195, USA				
COMMENT	On Jan 26, 2001 this sequence version replaced gi:10567930.				
	----- Genome Center				
	Center: University of Washington Genome Center				
	Web site: http://www.genome.washington.edu				
	Contact: uwgctg@u.washington.edu				
	----- Project Information				
	Center project name: HeaChr7				
	Center clone name: RP11-605P22 (djs708)				
	----- Summary Statistics				
	Sequencing vector: plasmid; X52328; 100% of reads				

Chemistry: Dye-terminator ET-amerham; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 217693 bases at least Q40  
 Consensus quality: 218145 bases at least Q30  
 Consensus quality: 218186 bases at least Q20  
 Insert size: 273875; 19.1% error; agarose-fp  
 Insert size: 218186; sum-of-coverage  
 Quality coverage: 8.30x in Q20 bases; agarose-fp  
 Quality coverage: 10.42x in Q20 bases; sum-of-coverage

Overlapping Sequences:

5': mapping in progress  
 3': RP11-243E12 (UMGC:djs156) AC018634, 6468-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI HindIII BglII

SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt

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663	<800	512	<800	5356	5585
122	<800	449	<800	1416	1421
174	<800	1059	1063	610	<800
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968	988	2594	2670	1982	2102
980	988	3852	3908	29	<800
10043	10231	915	918	2663	2719
2412	2471	5333	5315	5958	5921
3670	3625	4795	4869	448	<800

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359	<800	2624	2670	572	<800
57	<800	13428	13500	2139	2102
2128	2184	12540	12591	1593	1527
1087	1101	4819	4869	2049	2102
2839	2805	11280	11329	614	<800
2787	2805	840	918	7901	8084
5407	5309	9244	8985	619	<800
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349	<800	737	755	71	<800
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571	<800	8798	8985	6153	6135
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956	988	4946	4869	14	<800
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1821	1788	685	<800	10402	10380
2453	2471	1367	1406	300	<800
8955	9499	109	<800	5150	5294
1004	988	3608	3535	3195	3246
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4119	4107	357	<800	5869	5921
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4940	4902	957	918	655	<800
603	<800	5024	4869	1206	1270

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		2518	2471	1119	1195	19721	20141	
		4086	4107	709	<800	2331	2309	
		5916	5835	4907	4869	1940	1993	
		6995	6947	1161	1195	5574	5585	
		4667	4612	11292	11329	3867	3865	
		10434	10231	6699	6611	1268	1270	
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		374	<800	2400	2394	3636	3640	
Query Match	98.8%;	Score 927.8;	DB 9;	Length 218186;				
Best Local Similarity	99.8%;	Pred. No. 1.7e-232;						
Matches 929;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;				
QY	9	ATGTGACTTCCAGATATGCTGGCCACATATCTCCAGGAATTCCTTGGCATCTAT	68					
DB	133107	AGGTGACTTCCAGATATGCTGGCCACATATCTCCAGGAATTCCTTGGCATCTAT	133166					
QY	69	AGTGAACCCCACTTAATATGACCTTACTTATAGTCTTATTGGCGGCTGTGTGT	128					
DB	133167	AGTGAACCCCACTTAATATGACCTTACTTATAGTCTTATTGGCGGCTGTGTGT	133226					
QY	129	CATTTCATCTTTCTCTCTCTGTGAAATGAACACCCGGTCACTACCACTTGGCGGT	188					
DB	133227	CATTTCATCTTTCTCTCTCTGTGAAATGAACACCCGGTCACTACCACTTGGCGGT	133286					
QY	189	CATTAACTGT	248					
DB	133287	CATTAACTGT	133346					
QY	249	CCTCATCAAGAAAGACTTGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGATGCT	308					
DB	133347	CCTCATCAAGAAAGACTTGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGATGCT	133406					
QY	309	GCAATCCCACTATATCTTCACTTCTTATTTATTTGTGTGTGTGTGTGTGTGTGT	368					
DB	133407	GCAATCCCACTATATCTTCACTTCTTATTTATTTGTGTGTGTGTGTGTGTGTGT	133466					
QY	369	CATCTTCTCAAGTGAAGAACAAGTGAATTTCTACAGAAAAGTGTGTGTGTGTGT	428					
DB	133467	CATCTTCTCAAGTGAAGAACAAGTGAATTTCTACAGAAAAGTGTGTGTGTGTGT	133526					
QY	429	CAGTGTGTGATGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	488					
DB	133527	CAGTGTGTGATGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	133586					
QY	489	TGGAAATCCATGAGGATTAATGAGAGACATGTTTAAATTTCAAGAAAGCTTGTCT	548					
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QY	549	CACATATGTAAGAAATATCAATCAATATATGATGATGTTTGTATGAGCGGTGTGT	608					
DB	133647	CACATATGTAAGAAATATCAATCAATATATGATGATGTTTGTATGAGCGGTGTGT	133706					
QY	609	TCTGTGTGTTCTTCCAGGTCTTCAATTAATGTTGATGTGTGAGAGCTACGCACTTT	668					
DB	133707	TCTGTGTGTTCTTCCAGGTCTTCAATTAATGTTGATGTGTGAGAGCTACGCACTTT	133766					
QY	669	ACATATCCCAAGAGAGTTCTGGGCTCAAGTGAATAAATTTTATATAGGGGTCACTCT	728					
DB	133767	ACATATCCCAAGAGAGTTCTGGGCTCAAGTGAATAAATTTTATATAGGGGTCACTCT	133826					
QY	729	TGTTTGTTCCTTCCCTACCAAGTTCTTATGATCTATTAATTGATGTTGTGACGATTC	788					

DB	133827	TGTTTGTTCCTTCCCTACCAAGTTCTTATGATCTATTAATTGATGTTGTGACGATTC	133886					
QY	789	CAATGCTGTGAGAGAGAGTTGCATTTATTAAGAAATCTTTGATGTAAACAGCAT	848					
DB	133887	CAATGCTGTGAGAGAGAGTTGCATTTATTAAGAAATCTTTGATGTAAACAGCAT	133946					
QY	849	TACCTGCTATGATTTGCTTCTTGTGTTGGGGAGAGCATGTGTTTAAGAAAAGAT	908					
DB	133947	TACCTGCTATGATTTGCTTCTTGTGTTGGGGAGAGCATGTGTTTAAGAAAAGAT	134006					
QY	909	AATTGCTTATGGAATTTGTTTGTGCGGT	939					
DB	134007	AATTGCTTATGGAATTTGTTTGTGCGGT	134037					
RESULT 8								
LOCUS	CQ737895	1332 bp	DNA	linear	PAT 03-FEB-2004			
DEFINITION	Sequence 23829 from Patent WO02068579.							
ACCESSION	CQ737895							
VERSION	CQ737895.1	GI:42337355						
KEYWORDS								
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	1							
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.							
TITLE	Kite, such as nucleic acid arrays, comprising a majority of humenexons or transcripts, for detecting expression and other uses thereof							
JOURNAL	Patent: WO 02068579-A 23829 06-SEP-2002;							
PE	Corporation (NY) (US)							
FEATURES	Location/Qualifiers							
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ORIGIN								
Query Match	98.8%;	Score 927.4;	DB 6;	Length 1332;				
Best Local Similarity	99.9%;	Pred. No. 1.2e-232;						
Matches 928;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;				
QY	11	GTGACTTCCCAAGTATGCTGTGGCCACATATCTCCAGAAATTCCTTGCATCTATAG	70					
DB	401	GTGACTTCCCAAGTATGCTGTGGCCACATATCTCCAGAAATTCCTTGCATCTATAG	460					
QY	71	TGACACCCCACTTAATCAAGCTCTTACTTATAGTGTATTTGGCGGCTGTGTGTGT	130					
DB	461	TGACACCCCACTTAATCAAGCTCTTACTTATAGTGTATTTGGCGGCTGTGTGTGT	520					
QY	131	TTTTCATTTCTTCCCTGTTGAATGAACACCGGTCAGTGAACACATGGGGGTCA	190					
DB	521	TTTTCATTTCTTCCCTGTTGAATGAACACCGGTCAGTGAACACATGGGGGTCA	580					
QY	191	TTTAACTGT	250					
DB	581	TTTAACTGT	640					
QY	251	TGATCAAGAAAGT	310					
DB	641	TGATCAAGAAAGT	700					
QY	311	ACATCAACATGATGCTCAAGCTTCTTATTTATGTTGTGTGTGTGTGTGTGTGTGT	370					
DB	701	ACATCAACATGATGCTCAAGCTTCTTATTTATGTTGTGTGTGTGTGTGTGTGTGT	760					
QY	371	TCTTCTTCAAGTGAAGAACAAGTGAATTTCTACAGAAAAGTGTGTGTGTGTGTGT	430					
DB	761	TCTTCTTCAAGTGAAGAACAAGTGAATTTCTACAGAAAAGTGTGTGTGTGTGTGT	820					
QY	431	GTGCTGGCATGTGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	490					

|||||  
Db 821 GAGCTGGCAGTGGACGTGTATGTGATGTGTACCCCTGGTGTGCTCCCGGTATG 880  
QY 491 GAATCATAGAGAAATCAATGAGAGACTGTTTAAATTTCAAAAGAGCTTGCTTAA 550  
Db 881 GAATCATAGAGAAATCAATGAGAGACTGTTTAAATTTCAAAAGAGCTTGCTTAA 940  
QY 551 CATATGAAAAATCATCAATATATGATGATGATTTTGTGATAGCCGTGCTGATTC 610  
Db 941 CATATGAAAAATCATCAATATATGATGATGATTTTGTGATAGCCGTGCTGATTC 1000  
QY 611 TGTGTGCTTCCAGGCTTTCATCATTTATGTTGATGATGAGAGAGCTACGCCACTTTTAC 670  
Db 1001 TGTGTGCTTCCAGGCTTTCATCATTTATGTTGATGATGAGAGAGCTACGCCACTTTTAC 1060  
QY 671 TATCCACAGAGAGCTTGGGCTCAGCTGAAAAAACCCTATTTTAAAGGGGTGATCCTTG 730  
Db 1061 TATCCACAGAGAGCTTGGGCTCAGCTGAAAAAACCCTATTTTAAAGGGGTGATCCTTG 1120  
QY 731 TTTGTTTCCCTCCCTACAGATCTTAAAGATCTAATTAATGATGATGAGAGCTTCCCA 790  
Db 1121 TTTGTTTCCCTCCCTACAGATCTTAAAGATCTAATTAATGATGATGAGAGCTTCCCA 1180  
QY 791 ATGCTGTAGACAGAGAGTTGATTTTATPAACGAATCTTCTTGAAGTGAACAGCAATTA 850  
Db 1181 ATGCTGTAGACAGAGAGTTGATTTTATPAACGAATCTTCTTGAAGTGAACAGCAATTA 1240  
QY 851 GGTGCTATAGATTTGCTCTCTTGTGTTGGGGAGAGCAATGCTTAAAGCAAAAGATTA 910  
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Db 1301 TTGGCTTATGAAATGTGTTTGTGCGGT 1329

RESULT 9  
AX453412 1051 bp DNA linear PAT 06-JUL-2002  
LOCUS AX453412  
DEFINITION Sequence 1 from Patent W00244212.  
ACCESSION AX453412  
VERSION AX453412.1 GI:21712725  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Deleersnijder, W., Blockx, H. and de Moor, L.  
JOURNAL Human g-protein coupled receptor and uses thereof  
Patent: WO 0244212-A 1 06-JUN-2002;  
SOLVAY PHARMACEUTICALS B V (NL)  
FEATURES  
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ORIGIN  
Query Match 98.6%; Score 926.2; DB 6; Length 1051;  
Best Local Similarity 99.7%; Pired. No. 2.4e-232;  
Matches 928; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ATGTGACTTCCCAAGTATGCTGGCCAGAAATACCTCCAGAAATTCCTTGGATTCCTAT 68  
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QY 69 AGTGAACCCCACTTAATCAGCTTCTTACTTCAATAGCTTATTTGGCGGGCTGGGTGT 128  
Db 104 AGTGAACCCCACTTAATCAGCTTCTTACTTCAATAGCTTATTTGGCGGGCTGGGTGT 163  
QY 129 CATTTCCATTTCTTTCTCTCTGTTGAAAAATGAACCCCGGTGACAGACCAATGGCGGT 188  
Db 164 CATTTCCATTTCTTTCTCTCTGTTGAAAAATGAACCCCGGTGACAGACCAATGGCGGT 223  
QY 189 CATTAATCTGGAGTGTGTCACAGAGCTTTTCTGCTGACAGTGCATTTGCTTACCTTA 248  
Db 224 CATTAATCTGGAGTGTGTCACAGAGCTTTTCTGCTGACAGTGCATTTGCTTACCTTA 283  
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QY 369 CATCTTCTTCAAGTGCAGAAAGCAAGAGTGAATTTCTACAGAAAACTGCATGCTGTGGCTGC 428  
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LOCUS AC146385  
DEFINITION Pan troglodytes BAC clone RP43-126C6 from 7, complete sequence.  
ACCESSION AC146385  
VERSION AC146385.4 GI:46391241  
KEYWORDS HTG.

SOURCE  
ORGANISM Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
REFERENCE  
AUTHORS Kruchowski, S., Bielicki, L. and Haglund, K.  
TITLE The sequence of Pan troglodytes BAC clone RP43-126C6  
JOURNAL Unpublished (2001)  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (22-FEB-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-2004) Washington University School of Medicine,  
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
63108, USA  
COMMENT  
On Apr 15, 2004 this sequence version replaced gi:42734595.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@wustl.wustl.edu  
----- Summary Statistics  
Center project name: C\_P126C06  
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NOTICE:  
This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.  
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MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
http://genome.wustl.edu  
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SOURCE INFORMATION:  
The RP43-126C6 BAC library has been constructed by Chung-Li Shu. DNA  
was isolated from white blood cells obtained from a male chimpanzee  
(Pan troglodytes, 'Clint', Yerkes #C0471; birthdate: 6-6-80). The  
clone and detailed information can be obtained from Resgen  
(http://www.resgen.com) or Pieter de Jong and co-workers at  
http://www.bacpac.chori.org.  
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NEIGHBORING SEQUENCE INFORMATION:  
This sequence is the entire insert of the clone. This clone is  
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Location/Qualifiers  
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Query Match 98.3%; Score 923; DB 9; Length 162268;  
Best Local Similarity 99.5%; Pred. No. 3e-231;  
Matches 926; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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RESULT 11
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LOCUS      BD187510          918 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Novel Polypeptide.
ACCESSION BD187510
VERSION    BD187510.1 GI:32997249
KEYWORDS   JP 2003024082-A/1.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 918)
AUTHORS    Lee, H.
TITLE       Novel Polypeptide
JOURNAL     Patent: JP 2003024082-A 1 28-JAN-2003;
            Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)
COMMENT     OS Homo sapiens
            PN JP 2003024082-A/1
            PD 28-JAN-2003
            PE 17-JAN-2002 JP 2002008881
            PR 23-JAN-2001 GB 0101739.1
            PI Harland Lee
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Best Local Similarity 99.9%; Pred. No. 5.5e-229;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      145 CTCCTGTGTAATAAGAACCCGGTCAGTGAACCAACCATGCGGTCACTTAATCTTGATG 204
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QY      385 AAAGCAAAAGTGAATTTCTACAGAAAATGTCATGCTGTGCGCAGTGCCTGCAATGTG 444
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LOCUS      AX481576          918 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 1 from Patent EP1225183.
ACCESSION  AX481576
VERSION     AX481576.1 GI:22316490
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Harland, L.
TITLE       Human g-protein coupled receptor
JOURNAL     Patent: EP 1225183-A 1 24-JUL-2002;
            Pfizer Limited (GB) ; PFIZER INC. (US)
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Query Match      97.3%; Score 913.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 5.5e-229;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Sequence 3 from Patent WO0242461.			
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AX498180.1 GI:23343111			
KEYWORDS			
SOURCE			
ORGANISM			
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
AUTHORS			
TITLE			
1 Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.			
Endogenous and non-endogenous versions of human g protein-coupled			
receptors			
Patent: WO 0242461-A 3 30-WAY-2002;			
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Arena Pharmaceuticals, Inc. (US)			
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Db	301	CTCAGTTTCCATTTCTAATGTGTGATCTCTGTGCACAGATCTCTATTTTTCAGTGC	360	
QY	385	AAAGCAAAAGTGAATTTCTACAGAAAATGTCATCTGTGGCTGCAGTGTGGATGTGG	444	
Db	361	AAAGCAAAAGTGAATTTCTACAGAAAATGTCATCTGTGGCTGCAGTGTGGATGTGG	420	
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QY	505	TACATATGAGAGCACTGTTTAAATTTCACAAAGCTTGTTTCACATATGTGAATTC	564	
Db	481	TACATATGAGAGCACTGTTTAAATTTCACAAAGCTTGTTTCACATATGTGAATTC	540	
QY	565	ATCAACTATATGATATGATATTTTGTGATAGCGGTGCTGTGATTTCTGTTGGTCTTCAG	624	
Db	541	ATCAACTATATGATATGATATTTTGTGATAGCGGTGCTGTGATTTCTGTTGGTCTTCAG	600	
QY	625	GTCCTTCATCATTAATGTGATGTGTCAGAAAGTACGCCACTCTTACTATCCACAGAG	684	
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VERSION      BD105324.1 GI:22650898
KEYWORDS     MO 0196567-A/1
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE        Moriya, T., Ito, T., Shintani, Y. and Miyajima, N.
JOURNAL      Novel G protein-coupled receptor protein and its DNA
              Patent: WO 0196567-A 1 20-DEC-2001.
              TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
              SHINTANI, NOBUYUKI MIYAJIMA
COMMENT      OS Homo sapiens (human)
              PN MO 0196567-A/1
              PD 20-DEC-2001
              PF 14-JUN-2001 WO 2001JP005061
              PR 15-JUN-2000 JP 00P 184596,19-JUL-2000 JP 00P 223887 PI
              TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
              C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
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              PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC
              A61P29/00,
              PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/53, G01N33/566//
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Query Match 97.3%; Score 913.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 5.5e-229;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATGCGTCGACCAATACCTCCAGGAATTCCTCTGGATTCCTATAGTACACCCCACTTA 84
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QY 325 CTCACGTTCTATCTATGTGTGTGATCTGTGTCACCAAGTACCTCATCTTTCAAGTGC 384
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QY 625 GCTTCATCATATATGATGTGTGACAGAAAGTACGCCACTCTTTACTATCCACAGAG 684
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DB 781 AAGGTTGACATTTTAAACGAATCTTCTGAGTGAACAGCAATAGTGTATGATTTG 840
QY 865 CTCTCTTTTGTCTTGGGGAAAGCCATTTGTTAAGCAAAAGATATGCTTATGAAAT 924
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DB 901 TGTGTTTGTGCGCT 915

RESULT 15
AY288420 918 bp mRNA linear PRI 08-DEC-2003
LOCUS AY288420
DEFINITION Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete
cds.
ACCESSION AY288420
VERSION AY288420.1 GI:32165523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled
receptors lacking close relatives
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)
MEDLINE 22985413
PUBMED 14623098
REFERENCE 2 (bases 1 to 918)
AUTHORS Fredriksson, R., Hoglund, P. J., Gloriam, D. E., Lagerstrom, M. C. and
Schioth, H. B.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala
University, Box 593, Uppsala 75124, Sweden
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/db_xref="GI:32165524"
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FLFYVILVTRILYLPFKCKDKEFYRKLHAAVAASGMVTLVIVIVLVASRYGHEB
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YNEBHCFKHEKELAYTVKLIINWIVIFVIAVAILVFOVFIIMLVOKLRSLSH  
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Search completed: September 10, 2005, 07:21:31  
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## ORIGIN

Query Match 97.3%; Score 913.4; DB 9; Length 918;  
Best Local Similarity 99.9%; Pred. No. 5.5e-229;  
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 85 ATCAGCCTCTACTTCAATAGTCTTATGGGGGGCTGGGGGGTGCATTTCCATTCCTTTTC 144  
DB 61 ATCAGCCTCTACTTCAATAGTCTTATGGGGGGCTGGGGGGTGCATTTCCATTCCTTTTC 120

QY 145 CTCCTGTGAAAAATGAAACCCGGTCAGTACACACATGGCGGTCAATTAATTGGTGGTG 204  
DB 121 CTCCTGTGAAAAATGAAACCCGGTCAGTACACACATGGCGGTCAATTAATTGGTGGTG 180

QY 205 GTCACACAGCGTTTTCGTCTGACAGTGCATTTCGCTTGAACCTACCTCAAGAAAGACT 264  
DB 181 GTCACACAGCGTTTTCGTCTGACAGTGCATTTCGCTTGAACCTACCTCAAGAAAGACT 240

QY 265 TGGATGTTGGGGCGCCCTCTGCAAAATTTGTAGTGCATGTCGACATCCACATGTAC 324  
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DB 781 AAGGTGCAATTTATACGAAATCTTCTGAGTGTAAACAGCAATTAAGCTGTATGATTTG 840

QY 865 CTTCTCTTTGCTTTTGGGGGAGCCATGTTGTTAAGCAAAAGATAATGGCTTATGGAAT 924  
DB 841 CTTCTCTTTGCTTTTGGGGGAGCCATGTTGTTAAGCAAAAGATAATGGCTTATGGAAT 900

QY 925 TGTGTTTGTGCCGT 939  
DB 901 TGTGTTTGTGCCGT 915

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XX 28-FEB-2002; 2002MO-US006455.  
 PF 01-MAR-2001; 2001US-0272677P.  
 PR (MILL-) MILLENNIUM PHARM INC.  
 PA Gluckmann MA;  
 PI WPI; 2002-732793/79.  
 DR P-PSDB; AAO22919.  
 XX  
 XX New G-protein coupled receptor used in receptor assays as a target for  
 PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
 PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
 PT disorders.  
 XX  
 PS Claim 5; Page 101-103; 105pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide, which is a G-protein  
 CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
 CC receptor type proteins (GPCRs), designated the 93870 receptor. The  
 CC polypeptides, nucleic acid molecules and antibodies of the invention are  
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
 CC monitoring clinical trials or pharmacogenetics), or in methods of  
 CC treatment (e.g. therapeutic and prophylactic). They are useful in  
 CC treating and diagnosing conditions related to aberrant activity or  
 CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
 CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
 CC disorders, or bone marrow mononuclear disorders, as well as cellular  
 CC proliferative and/or differentiating disorders, hormonal disorders,  
 CC neurological disorders, cardiovascular disorders, viral diseases, liver  
 CC disorders, and pain and metabolic disorders. Conditions that can be  
 CC treated include cancer, diabetes mellitus, hypothyroidism, HIV, bacterial or  
 CC hyperthyroidism, reproductive or fertility disorders, multiple sclerosis,  
 CC viral meningitis, fungal meningoencephalitis, ataxia-telangiectasia,  
 CC Alzheimer's disease, Parkinson's disease, angina pectoris, myocardial  
 CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
 CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
 CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
 CC transgenic animals are useful for studying the function and/or activity  
 CC of a 93870 protein and for identifying and/or evaluating modulators of  
 CC 93870 activities. The polynucleotides of the invention can be used in  
 CC gene therapy. This polynucleotide sequence represents the 939 nucleotide  
 CC DNA of the human G-protein coupled receptor type protein of the invention  
 CC  
 XX  
 XX Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 939; DB 6; Length 939;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-268;  
 Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 361 AGATACCTCATCTTCTTCAAGTGCAAGCAAAAGTGAATTTCTACAGAAAACCTGATGCT 420  
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 DB 421 GTGGCTGCGACGTCGCGATGTGGAAGCTGTGATTTGCAATGTGTCACCCGTGTCG 480  
 QY 481 TCCCGGTATGGAATCCATGAGGATATACATGAGAGACCTGTTTAAATTTACAAAAG 540  
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 DB 481 TCCCGGTATGGAATCCATGAGGATATACATGAGAGACCTGTTTAAATTTACAAAAG 540  
 QY 541 CTTCCTTACACATATGTAAGAAATCATCAATATATATATGATTCATTTTGTCTATG 600  
 |||||  
 DB 541 CTTCCTTACACATATGTAAGAAATCATCAATATATATATGATTCATTTTGTCTATG 600  
 QY 601 GCTGTGATTCGTGTGTCTTCCAGGCTTCATCATATATGATGATGTCAGAAAGCTACG 660  
 |||||  
 DB 601 GCTGTGATTCGTGTGTCTTCCAGGCTTCATCATATATGATGATGTCAGAAAGCTACG 660  
 QY 661 CACTCTTACTATCCCAACGAGAGTTCTGGGCTGAGTGAACCTATTTTATAGAG 720  
 |||||  
 DB 661 CACTCTTACTATCCCAACGAGAGTTCTGGGCTGAGTGAACCTATTTTATAGAG 720  
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 DB 721 GTTCATCTTGTGTGTGTCTTCCCTACGAGTTCTTAAAGATCTATTAATGATGTGTG 780  
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 DB 781 AGCAGATTCGAAGCCGTGAGCAGCAAGGTGATTTTAAAGAAATCTTCTTGAGCTGA 840  
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 DB 841 ACAGCAATTAAGCTGATATGATTTGCTCTTGTCTTGGGGAAGCATTTGTTAAG 900  
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 DB 901 CAAAAGATTAATGCTTATGAGAAATGTGTGTGTGCGCT 939  
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 ID AAL53413 standard; cDNA; 1684 BP.  
 XX  
 XX AAL53413;  
 AC 12-DEC-2002 (first entry)  
 XX  
 DT 1684 nt cDNA of human G-protein coupled receptor type protein.  
 XX  
 XX Anti-HIV; cytostatic; antidiabetic; antiasrhmatic; antiinflammatory;  
 XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopelhic;  
 XX antibacterial; virucide; fungicide; anagestic; antiparkinsonian; GPCR;  
 XX cardiant; dermatological; antifertility; hepatotropic; antiallergic;  
 XX antiproliferative; ophthalmological; antiangiinal; anticholel; anticonvulsant;  
 XX antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;  
 XX 93870 receptor; immune; inflammatory disorder; platelet disorder;  
 XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;  
 XX cellular proliferative; differentiative disorder; viral disease; pain;  
 XX neurological disorder; cardiovascular disorder; cancer; diabetes mellitus; bacterial;  
 XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;  
 XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;  
 XX viral meningitis; fungal meningoencephalitis; multiple sclerosis;  
 XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;  
 XX Huntington's disease; heart failure; angina pectoris; dermatitis;  
 XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;  
 XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;  
 XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;





KM Parkinson's disease; Crohn's disease; constipation; infection;  
 KM gene therapy; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN W0200263004-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002W0-US003635.  
 XX  
 PR 07-FEB-2001; 2001US-0267322P.  
 PR 23-FEB-2001; 2001US-0271215P.  
 PR 08-MAR-2001; 2001US-0274551P.  
 PR 23-MAR-2001; 2001US-0278507P.  
 PR 30-MAR-2001; 2001US-0280597P.  
 PR 02-APR-2001; 2001US-0281107P.  
 PR 06-APR-2001; 2001US-0282121P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG,  
 PI Kallick DA, Gandhi AR, Malia NK, Arvizu C, Elliott VS, Hafalia AJA,  
 PI Ramkumar J, Pei J, Yang Y, Yue H, Reddy R, Butford N, Lu DAM,  
 PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA,  
 PI Warren BA, Yang J, Lee EA, Harland L,  
 XX  
 XX WPI; 2002-627557/67.  
 DR P-PSDB; AAB71325.  
 XX  
 PT New human G-protein coupled receptors (GCREC), useful for diagnosing or  
 PT treating a disease or condition associated with decreased expression or  
 PT over expression of functional GCREC e.g. cancer, Alzheimer's and  
 PT Parkinson's.  
 XX  
 PS Claim 113; Page 212-213; 239pp; English.  
 XX  
 CC This invention describes novel polypeptides which have anti-HIV,  
 CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,  
 CC hepatotropic, laxative, cerebroprotective, antiinflammatory, vinicide,  
 CC antibacterial, fungicide and protozoacide activity. The products of the  
 CC invention are useful for treating a disease or condition associated with  
 CC decreased expression or over expression of functional G-protein coupled  
 CC receptors (GCREC), while antibodies generated against the polypeptide of  
 CC the invention are useful for diagnosing a condition or disease associated  
 CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
 CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
 CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
 CC The compounds described in the invention can be used for gene therapy.  
 CC AAF8580-AAF8627 encode the GCREC proteins represented by AAB71322-  
 CC AAB71369, described in the disclosure of the invention  
 CC  
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 Best Local Similarity 99.9%; Pred. No. 1.7e-267;  
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 DB 795 GCTGATATCTGTTGGTCTTCCAGGCTTCTCATCATTTATGATGATGATGATGATGAT 854  
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 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.  
 XX  
 XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
 KM cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
 KM cerebroprotective; antiinflammatory; vinicide; antibacterial; fungicide;  
 KM protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
 KM Parkinson's disease; Crohn's disease; constipation; infection;  
 KM gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200263004-A2.  
 XX  
 PD 15-AUG-2002.  
 XX

PF 06-FEB-2002; 2002MO-US003635.  
XX  
PR 07-FEB-2001; 2001US-0267322P.  
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PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
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PI Kallik DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AJA;  
PI Rankumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;  
PI Grail RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee BA, Harland L;  
XX  
DR WPI; 2002-62757/67.  
XX P-PSDB; AAB71326.  
PT New human G-protein coupled receptors (GPRC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GPRCs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
PS Claim 114; Page 213; 239pp; English.  
XX  
XX This invention describes novel polypeptides which have anti-HIV,  
XX antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
XX hepatocytic, laxative, cerebroprotective, antiinflammatory, virucide,  
XX antibacterial, fungicide and protozoacide activity. The products of the  
XX invention are useful for treating a disease or condition associated with  
XX decreased expression or over expression of functional G-protein coupled  
XX receptors (GPRC), while antibodies generated against the polypeptide of  
XX the invention are useful for diagnosing a condition or disease associated  
XX with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,  
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
XX The compounds described in the invention can be used for gene therapy.  
XX AAF8580-AAF8627 encode the GPRC proteins represented by AAB71322-  
XX AAB71369, described in the disclosure of the invention  
SO Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;  
Query Match 98.8%; Score 928.2; DB 6; Length 1340;  
Best Local Similarity 99.7%; Pred. No. 9,4e-265;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7 AATGTGACTTCCCAAGTATGCTGCGCAATATCTCCAGAAATCTCTTGCGATCCT 66  
DB 205 ACAGGGGACTTCCCAAGTATGCTGCGCAATATCTCCAGAAATCTCTTGCGATCCT 264  
QY ATAGTGACCCCACTTATCAGGCTCTTACTGATAGTGCTTATTTGGCGGGCTGGGGCT 126  
DB 265 ATAGTGACCCCACTTATCAGGCTCTTACTGATAGTGCTTATTTGGCGGGCTGGGGCT 324  
QY 127 GTGATTTCAATTTTCTCTCTGCTGAATAATGAACCCCGTCAAGTACCAACATGGCG 186  
DB 325 GTGATTTCAATTTTCTCTCTGCTGAATAATGAACCCCGTCAAGTACCAACATGGCG 384  
QY 187 GTGATTTCAATTTTCTCTCTGCTGAATAATGAACCCCGTCAAGTACCAACATGGCG 246  
DB 385 GTGATTTCAATTTTCTCTCTGCTGAATAATGAACCCCGTCAAGTACCAACATGGCG 444  
QY 247 TACCTATCAAGAAGCTTGATGTTGGCTGCGCTTGCAGAAATTTGGAGTGCATG 306  
DB 445 TACCTATCAAGAAGCTTGATGTTGGCTGCGCTTGCAGAAATTTGGAGTGCATG 504  
QY 307 CTGCAATCCAGATGTAACCTCAAGTCTTATTTATGTGTGATCTGTGATCAACATAC 366  
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QY 367 CTGATCTTCTTCAAGTGCAGAAAGCAAAAGTGAATTCCTACAGAAAACCTGATGCTGCT 426  
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DB 805 ATTCTGTGTGCTTCCAGGCTTTCATCATATATGATATGCTGAGAGAGCTGACGCTCT 864  
QY 667 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACTATTTTATAGGGTCTATC 726  
DB 865 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACTATTTTATAGGGGCTATC 924  
QY 727 CTGTTTGTGCTTCTTCCCTACAGCTTCTTATGATCTATTTACTTGAATGTGACGCT 786  
DB 925 CTGTTTGTGCTTCTTCCCTACAGCTTCTTATGATCTATTTACTTGAATGTGACGCT 984  
QY 787 TCCATATCCCTGAGAGAGTGTGATTTTATTAAGAAATCTCTTGAAGTGAAGCA 846  
DB 985 TCCATATCCCTGAGAGAGTGTGATTTTATTAAGAAATCTCTTGAAGTGAAGCA 1044  
QY 847 ATTAGTGTGATGATTTGCTTCTTCTTCTTGGGGAAGCAATGTTTAAAGCAAAAG 906  
DB 1045 ATTAGTGTGATGATTTGCTTCTTCTTCTTGGGGAAGCAATGTTTAAAGCAAAAG 1104  
QY 907 ATTAGTGTGATGATTTGCTTCTTCTTCTTGGGGAAGCAATGTTTAAAGCAAAAG 939  
DB 1105 ATTAGTGTGATGATTTGCTTCTTCTTCTTGGGGAAGCAATGTTTAAAGCAAAAG 1137  
RESULT 5  
AAF8585  
ID AAF8585 standard; cDNA; 1460 BP.  
XX AC  
XX AAF8585;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Human GPRC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.  
XX  
XX GPRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
XX cytotactic; neuroprotective; antiparkinsonian; hepatocytic; laxative;  
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
XX Parkinson's disease; Crohn's disease; constipation; infection;  
XX gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200263004-A2.  
PD  
XX  
PD 15-AUG-2002.  
XX  
PF 06-FEB-2002; 2002MO-US003635.  
XX  
PR 07-FEB-2001; 2001US-0267322P.  
PR 23-FEB-2001; 2001US-0271215P.  
PR 08-MAR-2001; 2001US-0274551P.  
PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
PR 02-APR-2001; 2001US-0281107P.  
PR 06-APR-2001; 2001US-0282121P.

XX (INCY-) INCYTE GENOMICS INC.  
XX  
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG,  
PI Kalliock DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AJA,  
PI Ramkumar J, Pei J, Tang Y, Yue H, Reddy R, Bulford N, Lu DAM,  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA,  
PI Warren BA, Yang J, Lee EA, Harland L,  
XX  
DR WPI; 2002-627557/67.  
DR P-PSDS; AAB71327.  
XX  
PT New human G-protein coupled receptors (GCREC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GCREC e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
PS Claim 115; Page 213-214; 239pp; English.  
XX  
CC This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cyrostatic, neuroprotective, antiparkinsonian,  
CC hepatocrotic, laxative, cerebroprotective, antiinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GCREC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-  
CC AAB71369, described in the disclosure of the invention  
XX  
SQ Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;  
XX  
Query Match 98.8%; Score 928.2; DB 6; Length 1460;  
Best Local Similarity 99.7%; Pred. No. 9.8e-265;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 7 AAGTGTGACTTCCCAAGTATGCTGGCCACAAATACCTCCAGAAATCTCTTGCGATCCT 66  
DB 325 ACAGGTACTTCCCAAGTATGCTGGCCACAAATACCTCCAGAAATCTCTTGCGATCCT 384  
QY 67 ATAGTGACACCCCACTTAATCAGCCTTACTTCAATGCTTATGCGGGCGTGGGGT 126  
DB 385 ATAGTGACACCCCACTTAATCAGCCTTACTTCAATGCTTATGCGGGCGTGGGGT 444  
QY 127 GTCATTTCCATCTTTCTCTCTGCTGTAATAATGAACACCGGTCAAGTACACCATGGCG 186  
DB 445 GTCATTTCCATCTTTCTCTCTGCTGTAATAATGAACACCGGTCAAGTACACCATGGCG 504  
QY 187 GTCATTTAATCTTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACC 246  
DB 505 GTCATTTAATCTTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACC 564  
QY 247 TACCTCATCAAGAAGACTTGATGTTGGCTGCGCTTCGCAAAATTTGAGGCCANG 306  
DB 565 TACCTCATCAAGAAGACTTGATGTTGGCTGCGCTTCGCAAAATTTGAGGCCANG 624  
QY 307 CTGACATCCACATGTACTCAAGTTCCTTATTTCTATGTGATCTGTCACCATATAC 366  
DB 625 CTGACATCCACATGTACTCAAGTTCCTTATTTCTATGTGATCTGTCACCATATAC 684  
QY 367 CTCATCTTTCTTCAAGTCAAGAACAAAGTGAATTTCAAGAAAATGTCATGCTGGCT 426  
DB 685 CTCATCTTTCTTCAAGTCAAGAACAAAGTGAATTTCAAGAAAATGTCATGCTGGCT 744  
QY 427 GCCAGTCTGCGCATGTGAGCGCTGCTGATGTGATGTCATCCCGGTGCTCCCGG 486  
DB 745 GCCAGTCTGCGCATGTGAGCGCTGCTGATGTGATGTCATCCCGGTGCTCCCGG 804  
QY 487 TATGATTCATGAGTAATCAATGAGAGACCTGTTTAAATTTCAAAAAGCTTGCT 546

DB 805 TATGAAATCCATGAGAAATACAAATGAGAGACCTGTTTAAATTTCAAAAAGCTTGCT 864  
QY 547 TACACATATGTAATAATCATCAATATATGATAGTACATTTTGTATGCGGTGCTGG 606  
DB 865 TACACATATGTAATAATCATCAATATATGATAGTACATTTTGTATGCGGTGCTGG 924  
QY 607 ATTCTGTTGCTCTCCAGGTCTTCAATCATATGTTGATGAGTGCAGAAAGTACGCACCT 666  
DB 925 ATTCTGTTGCTCTCCAGGTCTTCAATCATATGTTGATGAGTGCAGAAAGTACGCACCT 984  
QY 667 TTACTATCCACACAGAGAGTCTGGGCTCACTGAAAAACCTATTTTATAGGGTCACT 726  
DB 985 TTACTATCCACACAGAGAGTCTGGGCTCACTGAAAAACCTATTTTATAGGGTCACT 1044  
QY 727 CTGTTGTTGCTCTCCAGGTCTTCAATCATATGTTGATGAGTGCAGAAAGTACGCACCT 786  
DB 1045 CTGTTGTTGCTCTCCAGGTCTTCAATCATATGTTGATGAGTGCAGAAAGTACGCACCT 1104  
QY 787 TCCAAATGCTGTAGACGAAAGTTCATTTTAAAGAAATCTCTGAGTAAACAGA 846  
DB 1105 TCCAAATGCTGTAGACGAAAGTTCATTTTAAAGAAATCTCTGAGTAAACAGA 1164  
QY 847 ATTAGCTGTATGATTTGCTCTTCTTGTCTTTGGGGGAAAGCATTGTTAAAGAAAG 906  
DB 1165 ATTAGCTGTATGATTTGCTCTTCTTGTCTTTGGGGGAAAGCATTGTTAAAGAAAG 1224  
QY 907 ATTAATGGCTTATGAAATTTGTTTGGCCCT 939  
DB 1225 ATTAATGGCTTATGAAATTTGTTTGGCCCT 1257  
XX  
RESULT 6  
AAH51009  
ID AAH51009 standard; DNA; 2525 BP.  
XX  
AC AAH51009;  
XX  
DT 28-AUG-2001 (first entry)  
XX  
DE Human nGPCR16 coding sequence #2.  
XX  
XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;  
XX signal transduction; schizophrenia; thyroid disorder; renal failure;  
XX rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
XX cardiovascular disease; proliferative disorder; hormonal disorder;  
XX neurological disorder; neuronal disorder; Alzheimer's disease; cancer;  
XX attention deficit-hyperactivity disorder; attention deficit disorder;  
XX Parkinson's disease; migraine; senile dementia; inflammatory disease;  
XX rheumatoid arthritis; autoimmune disorder; respiratory ailment;  
XX neuroprotective; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200136473-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000MO-US031581.  
XX  
XX 16-NOV-1999; 99US-0165838P.  
XX 17-NOV-1999; 99US-0166071P.  
XX 19-NOV-1999; 99US-0166678P.  
XX 28-DEC-1999; 99US-0173396P.  
XX 22-FEB-2000; 2000US-0184129P.  
XX 28-FEB-2000; 2000US-0185421P.  
XX 28-FEB-2000; 2000US-0185544P.  
XX 02-MAR-2000; 2000US-0186530P.  
XX 03-MAR-2000; 2000US-0186811P.  
XX 09-MAR-2000; 2000US-0188114P.  
XX 17-MAR-2000; 2000US-0190310P.  
XX 21-MAR-2000; 2000US-0190800P.  
XX 20-APR-2000; 2000US-0198568P.



PT New nucleic acids and polypeptides of the ng protein-coupled receptor,  
PT useful for treating or diagnosing a mental disorder or a disorder  
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or  
PT Parkinson's disease.

XX Example 1; Page 84-85; 244pp; English.

XX The invention discloses an isolated human polypeptide, and encoding  
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the  
CC ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the  
CC communication between cells and their environment and are characterised  
CC by a serpentine structure that passes through the cell membrane seven  
CC times, hence the reason such receptors are sometimes called seven  
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are  
CC useful for identifying an ngPCR allelic variant that correlates with a  
CC mental disorder, for isolating an antibody that binds to an epitope of  
CC the polypeptide, for identifying a compound that binds the polypeptide or  
CC polynucleotide and/or modulates its biological activity, for screening a  
CC human subject to diagnose a disorder, or a genetic predisposition to a  
CC disorder, affecting the brain or a genetic disposition to the disorder,  
CC for identifying compounds useful for the treatment of a mental disorder  
CC and for identifying a compound useful as a modulator of binding between  
CC ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also  
CC useful for inducing an immune response in a mammal. The nucleic acid or  
CC polypeptide is particularly useful, using gene therapy, for treating e.g.  
CC anxiety disorders, depression, bipolar disorder, schizophrenia,  
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's  
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also  
CC be used for treating diabetes, inflammation or wounds. The sequences  
CC presented in ABS70202-ABS70248, ABS70338 and ABS70243 are the DNAs  
CC encoding the ngPCRs (also referred to as beGPCRs)

XX Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

Query Match 98.8%; Score 928.2; DB 6; Length 2525;  
Best Local Similarity 99.7%; Pred. No. 1.3e-264;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AATATGACCTTCCAGATATGCTGGCCACCAATACCTCCAGAAATCTCTTGCATTCCT 66  
DB 9 ACAGGTGACCTTCCAGATATGCTGGCCACCAATACCTCCAGAAATCTCTTGCATTCCT 68  
QY 67 ATATGACACCCCACTTAATACCTCTTACTATAGTGTATTTATGCGGGGCTGTGGGT 126  
DB 69 ATATGACACCCCACTTAATACCTCTTACTATAGTGTATTTATGCGGGGCTGTGGGT 128  
QY 127 GTATTTCCATTTCTTCTCTCTGTGAAATGAAACCCGGTCACTGACACCACTGGCG 186  
DB 129 GTATTTCCATTTCTTCTCTCTGTGAAATGAAACCCGGTCACTGACACCACTGGCG 188  
QY 187 GTCAATTAACCTTGGTGGTGCACAGAGTTTCTGTGACAGTGCATTTGCTTGACC 246  
DB 189 GTCAATTAACCTTGGTGGTGCACAGAGTTTCTGTGACAGTGCATTTGCTTGACC 248  
QY 247 TACCTCATCAAGAAGACTTGATGTTGGGCTGCCCTTGCAAATTTGTGAGTGCATG 306  
DB 249 TACCTCATCAAGAAGACTTGATGTTGGGCTGCCCTTGCAAATTTGTGAGTGCATG 308  
QY 307 CTGCAATCCACATGTAACCTCAAGTTCCTATTCTATGTTGTATCTCTGTCACCAATAC 366  
DB 309 CTGCAATCCACATGTAACCTCAAGTTCCTATTCTATGTTGTATCTCTGTCACCAATAC 368  
QY 367 CTGATCTTCTTCAAGTGCAAAGCAAGTGAATTTCTACAGAAATCGCATGCTGGGCT 426  
DB 369 CTGATCTTCTTCAAGTGCAAAGCAAGTGAATTTCTACAGAAATCGCATGCTGGGCT 428  
QY 427 GCCAGTCTGGCATGTGACGCTGTGATTTGATTTGCTGATCCCTGTTGTCTCCCG 486  
DB 429 GCCAGTCTGGCATGTGACGCTGTGATTTGATTTGCTGATCCCTGTTGTCTCCCG 488  
QY 487 TATGGAATCCATGAGGAATTCATATGAGAGCACTGTTTAAATTTCACAAAAGCTTGCT 546  
DB 489 TATGGAATCCATGAGGAATTCATATGAGAGCACTGTTTAAATTTCACAAAAGCTTGCT 548

QY 547 TACACATATGTGAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTTGCTG 606  
DB 549 TACACATATGTGAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTTGCTG 608  
QY 607 ATTCTGTGTGCTTCCAGGCTTTCATCATATATGTTGATGTGACAGACCTACCACTCT 666  
DB 609 ATTCTGTGTGCTTCCAGGCTTTCATCATATATGTTGATGTGACAGACCTACCACTCT 668  
QY 667 TTACTATCCACACAGAGATTTGCGGCTCAGCTGAAAACCTATTTTATATAGGGTCAATC 726  
DB 669 TTACTATCCACACAGAGATTTGCGGCTCAGCTGAAAACCTATTTTATATAGGGTCAATC 728  
QY 727 CTGTGTTGTTTCTTCCCTACAGTTCCTTATAGATCTATTAATGAAATGTTGACGAT 786  
DB 729 CTGTGTTGTTTCTTCCCTACAGTTCCTTATAGATCTATTAATGAAATGTTGACGAT 788  
QY 787 TCCAAATGCTGTAGACACAGGTTGCATTTTAAACGAATCTTTGAGTGTAAACAGCA 846  
DB 789 TCCAAATGCTGTAGACACAGGTTGCATTTTAAACGAATCTTTGAGTGTAAACAGCA 848  
QY 847 ATTAGCTGTATGATTTGCTTCTTGTGTTGGGGAAGCCATTTGTTAAGCAAAAG 906  
DB 849 ATTAGCTGTATGATTTGCTTCTTGTGTTGGGGAAGCCATTTGTTAAGCAAAAG 908  
QY 907 ATAAATGGCTTATGGAATTTGTTTGGGCCGT 939  
DB 909 ATAAATGGCTTATGGAATTTGTTTGGGCCGT 941

#### RESULT 8

ADC86554  
ID ADC86554 standard; DNA; 113306 BP.

XX ADC86554;

XX 01-JAN-2004 (first entry)

XX Human GPCR gene SEQ ID NO:1007.

XX ds; gene; human; GPCR;

XX guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Arai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX P-PSDB; ADC86555.

XX New polynucleotide, useful for preparing a composition for treating a

XX patient in need of increased or suppressed activity or expression of the

XX guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 1007; 28bp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine

XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

XX the invention may have a use in gene therapy. The polynucleotide and

XX polypeptide are useful for preparing a composition for treating a patient

XX in need of increased or suppressed activity or expression of the

XX guanosine triphosphate-binding protein coupled receptor. The

CC polynucleotide sequences shown in AD85548-AD87616 encode GPCR's of the  
 CC invention.  
 XX  
 SQ Sequence 113306 BP, 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;  
 Query Match 98.8%; Score 927.8; DB 10; Length 113306;  
 Best Local Similarity 99.8%; Pred. No. 1.3e-263;  
 Matches 929; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ATGTGACCTTCCCAAGTATGCTGGCCCAACTACTCTCCAGAAATTCCTTGGCATCTAT 68  
 |||||  
 DB 11524 AGGGACCTTCCCAAGTATGCTGGCCCAACTACTCTCCAGAAATTCCTTGGCATCTAT 11583  
 |||||

QY 69 AGTACACCCCACTTATATGACCTCTACTCATAGTACTTATGGGGGGCTGGGGGGCT 128  
 |||||  
 DB 11584 AGTACACCCCACTTATATGACCTCTACTCATAGTACTTATGGGGGGCTGGGGGGCT 11643  
 |||||

QY 129 CATTTCATCTTCTTCTCTGCTGTAATAACACCCGGTCAGTGACCAACATGGCGGT 188  
 |||||  
 DB 11644 CATTTCATCTTCTTCTCTGCTGTAATAACACCCGGTCAGTGACCAACATGGCGGT 11703  
 |||||

QY 189 CATTAACTTGTGTGTGTCCACAGCGTTTTCGTGTCAGAGTCCATTTGGCTTACCTA 248  
 |||||  
 DB 11704 CATTAACTTGTGTGTGTCCACAGCGTTTTCGTGTCAGAGTCCATTTGGCTTACCTA 11763  
 |||||

QY 249 CCTCATCAAGAAAGACTTGGATGTTTGGGGCTGCCCTTTCGAAATTTGTGATGCCATGCT 308  
 |||||  
 DB 11764 CCTCATCAAGAAAGACTTGGATGTTTGGGGCTGCCCTTTCGAAATTTGTGATGCCATGCT 11823  
 |||||

QY 309 GCACATCCACATGATGATCTGACGTTCTCTATATGATGATCTGCTGTCACAGATACCT 368  
 |||||  
 DB 11824 GCACATCCACATGATGATCTGACGTTCTCTATATGATGATCTGCTGTCACAGATACCT 11883  
 |||||

QY 369 CATCTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAACTGTCATGCTGCTGC 428  
 |||||  
 DB 11884 CATCTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAACTGTCATGCTGCTGC 11943  
 |||||

QY 429 CAGTGTGCGATGATGAGACGCTGATGATGATGATGATGATGATGATGATGATGATGAT 488  
 |||||  
 DB 11944 CAGTGTGCGATGATGAGACGCTGATGATGATGATGATGATGATGATGATGATGATGAT 12003  
 |||||

QY 489 TGGATTCATGAGGAATATCAATGAGAGACACTGTTTAAATTTACAAAGAGCTTGCTTA 548  
 |||||  
 DB 12004 TGGATTCATGAGGAATATCAATGAGAGACACTGTTTAAATTTACAAAGAGCTTGCTTA 12063  
 |||||

QY 549 CACATATGTAATAATCATCACTATATGATGATGATGATGATGATGATGATGATGATGAT 608  
 |||||  
 DB 12064 CACATATGTAATAATCATCACTATATGATGATGATGATGATGATGATGATGATGATGAT 12123  
 |||||

QY 609 TCTGTGTGCTTCCAGGCTTTCATCATATGATGATGATGATGATGATGATGATGATGATGAT 668  
 |||||  
 DB 12124 TCTGTGTGCTTCCAGGCTTTCATCATATGATGATGATGATGATGATGATGATGATGATGAT 12183  
 |||||

QY 669 ACTATCCACACAGAGTTCGGGCTGACGTGAAAACCTATTTTATAGGGGTCAATCCT 728  
 |||||  
 DB 12184 ACTATCCACACAGAGTTCGGGCTGACGTGAAAACCTATTTTATAGGGGTCAATCCT 12243  
 |||||

QY 729 TGTGTGTGCTTCCCTTACAGTTCCTTATAGATCTATATGATGATGATGATGATGATGATGAT 788  
 |||||  
 DB 12244 TGTGTGTGCTTCCCTTACAGTTCCTTATAGATCTATATGATGATGATGATGATGATGATGAT 12303  
 |||||

QY 789 CAATGCTGTGACGACAGGTGCATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 848  
 |||||  
 DB 12304 CAATGCTGTGACGACAGGTGCATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 12363  
 |||||

QY 849 TACGTGCTATGATTTGCTTCTTGTCTTGGGGGAAGCATTTGTTTAAAGAAAGAT 908  
 |||||  
 DB 12364 TACGTGCTATGATTTGCTTCTTGTCTTGGGGGAAGCATTTGTTTAAAGAAAGAT 12423  
 |||||

QY 909 AATGCTTATGAAATGTTGTTTGGCCGT 939  
 |||||  
 DB 12424 AATGCTTATGAAATGTTGTTTGGCCGT 12454  
 |||||

RESULT 9  
 ID ABR87351 standard; cDNA; 1051 BP.  
 XX  
 AC ABR87351;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Human cDNA encoding G protein-coupled receptor IGS70.  
 XX  
 KM Human; sex; gene; G protein-coupled receptor; GPCR; IGS70; CNS;  
 KM psychiatric disorder; central nervous system disorder; schizophrenia;  
 KM Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;  
 KM heart failure; angina pectoris; myocardial infarction; kidney disease;  
 KM renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;  
 KM inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;  
 KM asthma; infection; human immunodeficiency virus infection; HIV; diabetes;  
 KM osteoporosis; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 60..977  
 FT /tag= a  
 FT /product= "GPCR IGS70"  
 XX  
 PN MO200244212-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 23-NOV-2001; 2001MO-EP013706.  
 XX  
 PR 30-NOV-2000; 2000EP-00204280.  
 XX  
 PR 05-DEC-2000; 2000US-0251045P.  
 XX  
 PA (SOLV ) SOLVAY PHARM BV.  
 XX  
 PI Deleersnijder W, Blockx H, De Moor L,  
 XX  
 DR WPI; 2002-527703/56.  
 XX  
 PT P-PSDB; AAN99179.  
 XX  
 PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating  
 PT dysfunctions, disorders or disease related to lung, bone marrow, spinal  
 PT cord immune system.  
 XX  
 PS Claim 1; Page 6; 58pp; English.

XX The invention relates to a G protein-coupled receptor (GPCR) IGS70  
 CC polypeptide including sequences that are 98-99.6% identical. Also  
 CC included are the polynucleotide encoding IGS70 (including sequences 98-  
 CC 99.6% identical to the polynucleotide or the DNA insert contained in  
 CC plasmid CBS 109818), a hybridisation probe derived from the  
 CC polynucleotide, a DNA or RNA expression system producing IGS70, a host  
 CC comprising the expression system, IGS70 receptor membrane preparation  
 CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is  
 CC useful for diagnosing a disease or a susceptibility to disease in a  
 CC subject related to expression or activity of the IGS70 polypeptide in a  
 CC subject by determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding IGS70 in the genome of the subject in a  
 CC sample derived from the subject. IGS70 is also useful identifying agonist  
 CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified  
 CC ant/agonists are useful for treating psychiatric and central nervous  
 CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,  
 CC multiple sclerosis, anxiety, cardiovascular diseases such as heart  
 CC failure, angina pectoris, myocardial infarction, kidney disease such as  
 CC renal failure, gastrointestinal disorders such as irritable bowel  
 CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,  
 CC inflammation, cancer, asthma, infection (such as bacterial, viral,  
 CC fungal, protozoal) especially human immunodeficiency virus infection  
 CC (HIV), diabetes, osteoporosis and allergies. The present sequence encodes  
 CC the human GPCR IGS70



XX Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 98.6%; Score 926.2; DB 6; Length 1051;  
Best Local Similarity 99.7%; Pred. No. 3.2e-264;  
Matches 928; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 9 ATGTGACTTCCCAAGATGCTGGCCACATATCTCCAGGAATTCCTTGGATCCTAT 68
DB 44 AGGTGACTTCCCAAGATGCTGGCCACATATCTCCAGGAATTCCTTGGATCCTAT 103
QY 69 AGTGACACCCCACTTATATCAGCTCTTATCATATGCTTATTTGGGGCTGGTGGAT 128
DB 104 AGTGACACCCCACTTATATCAGCTCTTATCATATGCTTATTTGGGGCTGGTGGAT 163
QY 129 CATTTTCATTTCTTTCTCTCTGCTGTAATAATGAACACCCGGTCACTGACCAATGCGGT 188
DB 164 CATTTTCATTTCTTTCTCTCTGCTGTAATAATGAACACCCGGTCACTGACCAATGCGGT 223
QY 189 CATTAATCTGGTGGTGGTCCAGACGCTTTTCTGCTGACAGTGCATTTGCTTGAACCTA 248
DB 224 CATTAATCTGGTGGTGGTCCAGACGCTTTTCTGCTGACAGTGCATTTGCTTGAACCTA 283
QY 249 CCTCATCAAGAAAGACTTGATGTTGGGCTGCCCTTCTGCAATTTTGTAGTGCATGCT 308
DB 284 CCTCATCAAGAAAGACTTGATGTTGGGCTGCCCTTCTGCAATTTTGTAGTGCATGCT 343
QY 309 GCACATCCACATATCTACCTACGTTCTATTTCTATGCTGATCTGCTGACCAAGATACCT 368
DB 344 GCACATCCACATATCTACCTACGTTCTATTTCTATGCTGATCTGCTGACCAAGATACCT 403
QY 369 CATCTTCTTCAAGTGCAGAAAGACAAAGTGAATCTACAGAAAACCTGATCTGCTGCTG 428
DB 404 CATCTTCTTCAAGTGCAGAAAGACAAAGTGAATCTACAGAAAACCTGATCTGCTGCTG 463
QY 429 CAGTGTGCTGATGTGACGCTGTGATGTCATTTGTGATGTCATTTGTGCTGCTGCTG 488
DB 464 CAGTGTGCTGATGTGACGCTGTGATGTCATTTGTGATGTCATTTGTGCTGCTGCTG 523
QY 489 TGGAAATCCATGAGAAATACATAGAGAGCACTGTTTAAATTTCAAAAGAGCTTCTTA 548
DB 524 TGGAAATCCATGAGAAATACATAGAGAGCACTGTTTAAATTTCAAAAGAGCTTCTTA 583
QY 549 CACATATGGAATAATCATCACTATATGATGATCATTTTGTGATGCTGCTGCTGAT 608
DB 584 CACATATGGAATAATCATCACTATATGATGATCATTTTGTGATGCTGCTGCTGAT 643
QY 609 TCTGTGTGCTTTCAGGCTTTCATCATATGATGATGCTGACAGAGCTACGCCACTTT 668
DB 644 TCTGTGTGCTTTCAGGCTTTCATCATATGATGATGCTGACAGAGCTACGCCACTTT 703
QY 669 ACTATCCACACAGAGGTTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGTCACTCT 728
DB 704 ACTATCCACACAGAGGTTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGTCACTCT 763
QY 729 TGTGTGTGCTTCCCTACAGGTTCTTATAGATCTTATCTTGAATGTTGTGAGCATTC 788
DB 764 TGTGTGTGCTTCCCTACAGGTTCTTATAGATCTTATCTTGAATGTTGTGAGCATTC 823
QY 789 CAATGCTGTAGCAGAGGTTCAATTTTATGAAGAATCTTCTGATGCTAACAGCAAT 848
DB 824 CAATGCTGTAGCAGAGGTTCAATTTTATGAAGAATCTTCTGATGCTAACAGCAAT 883
QY 849 TAGCTGTATGATTTGCTTCTTTGCTTGGGGGAGCCATTTGTTTAAAGAAAGAT 908
DB 884 TAGCTGTATGATTTGCTTCTTTGCTTGGGGGAGCCATTTGTTTAAAGAAAGAT 943
QY 909 AATTGGCTATGAAATTTGTTTGTGCGGT 939
DB 944 AATTGGCTATGAAATTTGTTTGTGCGGT 974

```

RESULT 10

```

AAL44713
ID AAL44713 standard; DNA; 918 BP.
XX AC AAL44713;
XX DT 03-MAY-2002 (first entry)
XX DE Human testis originated G-protein coupled receptor TGR10 coding sequence.
XX KW Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
XX KW cytostatic; immunomodulator; cardiatic; neuroprotective; gene therapy;
XX KW inflammation; nervous system disease; circulatory system disease; cancer;
XX KW metabolic disease; immunological disease; gastrointestinal disease; gene;
XX KW ds.
XX OS Homo sapiens.
XX FH Key
XX FT CDS Location/Qualifiers
XX FT 1..918
XX FT /tag= a
XX FT /product= "TGR10"
XX PN WO200196567-A1.
XX PD 20-DEC-2001.
XX PF 14-JUN-2001; 2001WO-0P005061.
XX PR 15-JUN-2000; 2000JP-00184596.
XX PR 19-JUL-2000; 2000JP-00223887.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Moriya T, Ito T, Shintani Y, Miyajima N;
XX DR WPI; 2002-098071/13.
XX DR P-PSDB; AAM48398.
XX PT Human testis-originated G protein-coupled receptor protein TGR10 and
XX PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.
XX PT diseases of central nervous system, inflammations and diseases of
XX PT circulatory system.
XX PS Claim 5; Page 99; 110pp; Japanese.
XX CC The present invention provides the protein and coding sequences of a
XX CC novel human testis-originated G protein-coupled receptor protein TGR10.
XX CC The sequences can be used in the development of drugs for the treatment
XX CC of diseases of the central nervous system, inflammations, diseases of the
XX CC circulatory system, cancer, metabolic diseases, immunological diseases,
XX CC and diseases of the gastrointestinal system. The present sequence is the
XX CC coding sequence of the invention
XX SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Query Match 97.3%; Score 913.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 1.9e-260;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 ATGCTGGCCACAATACCTCCAGAAATTCCTTGCATCTTATAGTACACCCCACTTA 84
DB 1 ATGCTGGCCACAATACCTCCAGAAATTCCTTGCATCTTATAGTACACCCCACTTA 60
QY 85 ATCAGCTTACTTATATGATGCTTATTTGGCGGGCTGTGGGTGATTTCCATTTCTTTTC 144
DB 61 ATCAGCTTACTTATATGATGCTTATTTGGCGGGCTGTGGGTGATTTCCATTTCTTTTC 120
QY 145 CTCCTGGTGAATAATGAACCCGGTCACTGACCAACATGCGGCTCATTAATCTTGGTGGT 204
DB 121 CTCCTGGTGAATAATGAACCCGGTCACTGACCAACATGCGGCTCATTAATCTTGGTGGT 180
QY 205 GTCCACAGCGTTTTCTGTGACAGTGCATTTGCTTGAACCTACCTATCAAGAACT 264

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Dp	181	GTCCACAGGGTTTTCGTGCGACAGTGCCATTTTCGCTGACCTACCTCATCAAGAAACT	240
Qy	265	TGGAATTTGGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCATGTAC	324
Dp	241	TGGAATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCATGTAC	300
Qy	325	CTCAGGTCCTAATTCATAGTGGGATCCGTGTCACCGATACCTCATCTTCTTCAAGTGC	384
Dp	301	CTCAGGTCCTAATTCATAGTGGGATCCGTGTCACCGATACCTCATCTTCTTCAAGTGC	360
Qy	385	AAAGCAAAAGTGGAAATTTACAGAAAACTGCATGCTGTGGCTGCGATGCTGCATGTGG	444
Dp	361	AAAGCAAAAGTGGAAATTTACAGAAAACTGCATGCTGTGGCTGCGATGCTGCATGTGG	420
Qy	445	ACGCTGTGATTTGTCAATGTGGTACCCCTGTTGTCTCCCGATAGAAATCCATGAGAA	504
Dp	421	ACGCTGTGATTTGTCAATGTGGTACCCCTGTTGTCTCCCGATAGAAATCCATGAGAA	480
Qy	505	TACAAATGAGGACACGTGTTTAAATTTCCAAAGAGCTTGCTTACCATATGTGAAATC	564
Dp	481	TACAAATGAGGACACGTGTTTAAATTTCCAAAGAGCTTGCTTACCATATGTGAAATC	540
Qy	565	ATCACTATAATATAGTACATTTTGTGCATAGACCGTGTGATGTTGTTGGCTTCCAG	624
Dp	541	ATCACTATAATATAGTACATTTTGTGCATAGACCGTGTGATGTTGTTGGCTTCCAG	600
Qy	625	GTCCTCATCATATATGTGATGATGATGTCAGAAAGCTACGCCATCTTATCTATCCACAGAG	684
Dp	601	GTCCTCATCATATATGTGATGATGATGTCAGAAAGCTACGCCATCTTATCTATCCACAGAG	660
Qy	685	TTCTGGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTGTTGTTTCTTCCC	744
Dp	661	TTCTGGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTGTTGTTTCTTCCC	720
Qy	745	TACCACTCTTAAGGATCTATACTTGAATGTGTGATAGGCAATTCGAATGCCGTACACGC	804
Dp	721	TACCACTCTTTAGGATCTATTACTTGAATGTGTGATAGGCAATTCGAATGCCGTACACGC	780
Qy	805	AAGGTGCAATTTATACGAAATCTTCTAGAGTGTAACGCAATTAGCTGATGATTTG	864
Dp	781	AAGGTGCAATTTTATACGAAATCTTCTAGAGTGTAACGCAATTAGCTGATGATTTG	840
Qy	865	CTTCTCTTTGCTTTTGGGGGAAAGCAATGAGTTTAAAGCAAAAGATATTTGGCTTATGAAAT	924
Dp	841	CTTCTCTTTGCTTTTGGGGGAAAGCAATGAGTTTAAAGCAAAAGATATTTGGCTTATGAAAT	900
Qy	925	TGTGTTTTGTGCGCT 939	
Dp	901	TGTGTTTTGTGCGCT 915	

OS	XX	Key	Location/Qualifiers
XX	XX	FT	
XX	XX	CDS	1..918
RESULT 11			
ABA00160			
ID	ABA00160	standard; cDNA; 918	BP.
XX			
AC	ABA00160;		
XX			
DT	15-NOV-2002	(first entry)	
XX			
DE	PFI-021 cDNA.		
XX			
KM	Gene; human; G-protein coupled receptor; GPCR; PFI-021;		
KM	peripheral blood mononuclear cell; PMBC; breast; inflammation; allergy;"		
KM	respiratory; neurology; psychology; urogenital disease; cancer; tissue repair;		
KM	reproductive dysfunction; sexual dysfunction; cancer; tissue repair;		
KM	dermatology; skin pigmentation; photogelns; frailty; osteoporosis;		
KM	metabolic disease; cardiovascular disease; sleep disorder; hair loss;		
KM	gastrointestinal disease; anti-infection; sensory organ disorder; ss.		
XX			
OS	Homo sapiens.		

FT		/tag= "a"
FT		/product= "PFI-021"
XX		
PN	EPI225183-A2.	
XX		
PD	24-JUL-2002.	
XX		
PF	09-JAN-2002; 2002EP-00250128.	
XX		
PR	23-JAN-2001; 2001GB-00001739.	
XX		
PA	(PFI2 ) PFIZER LTD.	
XX	(PFI2 ) PFIZER INC.	
P1	Harland L;	
DR	WPI; 2002-601226/65.	
XX		
DR	P-PsDB; AAG79446.	
XX		
PT	New human G-protein coupled receptor involved in signal transduction,	
PT	useful to treat disorders associated with its expression or activity, such	
XX	as inflammation, allergy and cancer.	
PS	Claim 1; Fig 1; 8bp; English.	
CC	This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.	
CC	Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA	
CC	libraries from peripheral blood mononuclear cells. Two ESTs have been	
CC	identified in libraries derived from breast mRNA. PFI-021 and the	
CC	corresponding cDNA are used to treat a patient needing altered activation	
CC	or expression of a GPCR, such as inflammation, allergy and respiratory,	
CC	neurology, psychology, urogenital disease, reproductive and sexual	
CC	dysfunction/disorders, cancer, tissue repair, dermatology, skin	
CC	pigmentation disorders, photogeising, frailty, osteoporosis, metabolic	
CC	diseases, cardiovascular disease, gastro-intestinal disease, anti-	
CC	infection, sensory organ disorders, sleep disorders and hair loss	
XX		
SQ	Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;	
	Query Match 97.3%; Score 913.4; DB 6; Length 918;	
	Best Local Similarity 99.9%; Pred. No. 1.9e-260;	
	Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	25 ATGCGTGGCCCAATACCTCCAGGAATTCTTTGCATCCTATATGTAGACCCCATTA 84	
Db	1 ATGCGTGGCCCAATACCTCCAGGAATTCTTTGCATCCTATATGTAGACCCCATTA 60	
OY	85 ATCAGCCTCTAATCTAATGACTTATTGGGGGGCTGGTGAGTCATTTCCATTCTTTTC 144	
Db	61 ATCAGCCTCTAATCTAATGACTTATTGGGGGGCTGGTGAGTCATTTCCATTCTTTTC 120	
OY	145 CTCTGGTGAATAAGAACACCCGGTCAAGTACCAACATGGCGGTCATTAACTTGGTGTG 204	
Db	121 CTCTGGTGAATAAGAACACCCGGTCAAGTACCAACATGGCGGTCATTAACTTGGTGTG 180	
OY	205 GTCCACAGCGTTTTTCTGTGACAGTGCATTTTGGTCTGACCTTACCTATCAAGAAGACT 264	
Db	181 GTCCACAGCGTTTTTCTGTGACAGTGCATTTTGGTCTGACCTTACCTATCAAGAAGACT 240	
OY	265 TGAGATGTTGGGGCTGCCCTTCTGCATTTTGTGAGTCCATGCTGCACATCCACATGTAC 324	
Db	241 TGAGATGTTGGGGCTGCCCTTCTGCATTTTGTGAGTCCATGCTGCACATCCACATGTAC 300	
OY	325 CTACGTTTCTAATCTATATGAGTGAATCTTGGTACCAGATACCAATCTTCCAATGTC 384	
Db	301 CTACGTTTCTAATCTATATGAGTGAATCTTGGTACCAGATACCAATCTTCCAATGTC 360	
OY	385 AAAGACAAGATGGAATTTCTACAGAAAATGTCATGCTGTGCTGCCAGTGTGGCATGTGG 444	
Db	361 AAAGACAAGATGGAATTTCTACAGAAAATGTCATGCTGTGCTGCCAGTGTGGCATGTGG 420	
OY	445 ACGCTGGTATTTGTCATTGTGTGTAACCCCTGTGTTGTCTCCGGTATGGAATTCATGAGAA 504	

XX	RESULT 12
XX	ABT04867
ID	ABT04867 standard; cDNA, 918 BP.
XX	
AC	ABT04867;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	Human G protein coupled receptor hRUP29 coding sequence.
XX	
KW	Human; G-protein coupled receptor; GPCR, hRUP28, hRUP29, hRUP30, hRUP31, hRUP32, hRUP33, hRUP34, hRUP35, hRUP36, hRUP37; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200242461-A2.
XX	
PD	30-MAY-2002.
XX	
PF	26-NOV-2001, 2001WO-US044386.
XX	
PR	27-NOV-2000; 2000US-0253304P.
PR	12-DEC-2000; 2000US-0253366P.
PR	20-FEB-2001; 2001US-0270266P.
PR	20-FEB-2001; 2001US-0270286P.
PR	06-APR-2001; 2001US-0282032P.
PR	06-APR-2001; 2001US-0282356P.
PR	06-APR-2001; 2001US-0282358P.
PR	06-APR-2001; 2001US-0282365P.
PR	14-MAY-2001; 2001US-0290917P.
PR	31-JUL-2001; 2001US-0309208P.
XX	
PA	(AREN-) ARENA PHARM INC.
XX	
PI	Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX	
WI	WPI, 2002-566565/60.
DR	P-PSDB; AB04069.

XX	Novel endogenous and non-endogenous versions of G protein-coupled
PT	receptor useful for identification of candidate compounds as receptor
PT	agonists or antagonists for use as therapeutic agents.
XX	
PS	Claim 7; Page 56-57; 84pp; English.
XX	
CC	The present invention provides the protein and coding sequences of
CC	several human G-protein coupled receptors (GPCRs). These can be used in
CC	the identification of candidate compounds as receptor agonists or inverse
CC	agonists having applicability as therapeutic agents. The present sequence
CC	is a GPCR coding sequence of the invention
XX	
SQ	Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
	Query Match 97.3%; Score 913.4; DB 6; Length 918;
	Best Local Similarity 99.9%; Pred. No. 1.9e-260;
	Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	25 ATGCTGGCCACAAATACCTCCAGAAATTCCTTGGGATCTTAAAGTGAACACCCCACTTA 84
DB	1 ATGCTGGGCCAATAACCTCCAGAAATTCCTTGGGATCTTAAAGTGAACACCCCACTTA 60
QY	85 ATACACCTCTACTTCAATAGTGGTTATTGGCCGGGCTGGTGGGGTCAATTCATCTTTTC 144
DB	61 ATACACCTCTACTTCAATAGTGGTTATTGGCCGGGCTGGTGGGGTCAATTCATCTTTTC 120
QY	145 CTCCTGGTGAATAATGAACACCCGGGTCAGTGAACACACATGGCCGATTAATCTGTGGTGTG 204
DB	121 CTCCTGGTGAATAATGAACACCCGGGTCAGTGAACACACATGGCCGATTAATCTGTGGTGTG 180
QY	205 GTCCACAGCGTTTTCTGCTGACAGTGGCCATTTGGCTTGACCTCATCAAGAAAGACT 264
DB	181 GTCCACAGCGTTTTCTGCTGACAGTGGCCATTTGGCTTGACCTCATCAAGAAAGACT 240
QY	265 TGGATGTTTGGGCTGCCCTTCTGCAAAATTGTAAGTGCATGCTGACATCCACATGATAC 324
DB	241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTGTAAGTGCATGCTGACATCCACATGATAC 300
QY	325 CTCACGTTCTTATTATGTGGTGAATCCGTCACACAGATACCTCATCTTCTTCAAGTGC 384
DB	301 CTCACGTTCTTATTATGTGGTGAATCCGTCACACAGATACCTCATCTTCTTCAAGTGC 360
QY	385 AAAAGCAAAATGGAATTCTACAGAAAATCTGATCTGTGGCTGCCAGTGCCTGGCATGTGG 444
DB	361 AAAAGCAAAATGGAATTCTACAGAAAATCTGATCTGTGGCTGCCAGTGCCTGGCATGTGG 420
QY	445 ACGCTGGGATGTGATGTGTGTACCCCTGTGTGTCTCCCGGTATGGAAATCCATATAGGAA 504
DB	421 ACGCTGGGATGTGATGTGTGTGTACCCCTGTGTGTCTCCCGGTATGGAAATCCATATAGGAA 480
QY	505 TACAAATGAGAGACACGTTTTTAAATTTTCACAAAAGACCTGGCTTACATATGGAANAATC 564
DB	481 TACAAATGAGAGACACGTTTTTAAATTTTCACAAAAGACCTGGCTTACATATGGAANAATC 540
QY	565 ATCAACTATATGATGTGATCTTTTGTGCAATAGCCGTTGTCTGATCTGTGTGCTTCCAG 624
DB	541 ATCAACTATATGATGTGATCTTTTGTGCAATAGCCGTTGTCTGATCTGTGTGCTTCCAG 600
QY	625 GTCTTCATCATATTGTTGATGTGCAAGAACTACGCACTTTTACTATATCCACACAGAG 684
DB	601 GTCTTCATCATATTGTTGATGTGCAAGAACTACGCACTTTTACTATATCCACACAGAG 660
QY	685 TTCCTGGGCTCAGCTGAAAAAAGCTATTTTATATGGGGTATCCGTGTGTTTCCATCC 744
DB	661 TTCCTGGGCTCAGCTGAAAAAAGCTATTTTATATGGGGTATCCGTGTGTGTTTCCATCC 720
QY	745 TACCAAGTCTTAAAGATCTATTTACTTGAATGTTGTGACGATTTCCATCTGCTGACAGC 804
DB	721 TACCAAGTCTTAAAGATCTATTTACTTGAATGTTGTGACGATTTCCATCTGCTGACAGC 780
QY	805 AAGGTGCAATTTTATACGAAATCTTCTTGAAGTGTATACGCAATTAAGTGTATGATTTG 864

Db 781 AAGTTGCAATTTTAAACGAAATCTTGAAGTGAACAGCAATTAGCTGATGATTTG 840  
QY 865 CTCTCTTTGCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATGCTTATGCAAT 924  
Db 841 CTCTCTTTGCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATGCTTATGCAAT 900  
QY 925 TGTGTTTGTGCGGT 939  
Db 901 TGTGTTTGTGCGGT 915

RESULT 13  
ABZ59171  
ID ABZ59171 standard; DNA; 918 BP.  
XX  
AC ABZ59171;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Human TGR343 protein encoding DNA.  
XX  
KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;  
KW TGR35; antidiabetic; neuroprotective; cerebroprotective; nephrotoxic;  
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;  
KW immunosuppressive; antiinflammatory; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..918  
FT /\*tag= a  
FT /product= "TGR343"  
XX  
PN W02003004678-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 01-JUL-2002; 2002WO-US020860.  
XX  
PR 03-JUL-2001; 2001US-0302800P.  
XX  
PA (TUL- ) TULARIK INC.  
XX  
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;  
XX  
DR WPI; 2003-210368/20.  
DR P-PSDB; ABP71378.  
XX  
XX  
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
PT nephrolithiasis.  
XX  
PS Claim 7; Page 61; 74pp; English.  
XX  
XX The invention provides new G-protein coupled receptor (GPCR) polypeptides  
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding  
CC polynucleotides. The polypeptides can be expressed by standard DNA  
CC recombinant methodology. The polypeptides are useful for screening or  
CC identifying modulators of GPCR or signal transduction. The modulators of  
CC signal transduction are useful for treating or preventing TGR-associated  
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
CC polypeptides are useful as targets for diagnosing or treating e.g.  
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,  
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute  
CC inflammatory dermatoses. The present sequence represents a human TGR343  
CC protein encoding DNA  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 25 ATGCTGGCCCAATATCTCCAGGAATTCCTTTCGATCTTATAGTACACCCCACTTA 84  
Db 1 ATGCTGGCCCAATATCTCCAGGAATTCCTTTCGATCTTATAGTACACCCCACTTA 60  
QY 85 ATGAGCCCTTATCTTATAGTCTTATGAGGGGCTGGTGGGTGATCTTTCATCTTTTC 144  
Db 61 ATGAGCCCTTATCTTATAGTCTTATGAGGGGCTGGTGGGTGATCTTTCATCTTTTC 120  
QY 145 CTCTGTGTAATAATGAACACCCGGTCAGTACACCAACATGCGGCTTAACTTGATG 204  
Db 121 CTCTGTGTAATAATGAACACCCGGTCAGTACACCAACATGCGGCTTAACTTGATG 180  
QY 205 GTCCACAGCGTTTTTCTGCTGACAGTCCATTTGCTTGAACCTACCTCATCAAGAACT 264  
Db 181 GTCCACAGCGTTTTTCTGCTGACAGTCCATTTGCTTGAACCTACCTCATCAAGAACT 240  
QY 265 TGGATGTTGGGGCTGCGCCCTCTGCAATTTGTAGTGGCAATGCTGCAATCCACATGAC 324  
Db 241 TGGATGTTGGGGCTGCGCCCTCTGCAATTTGTAGTGGCAATGCTGCAATCCACATGAC 300  
QY 325 CTCACGTTCTTATCTTATGATGATCTGCTGACACGATACCTCATCTTCAAGTGC 384  
Db 301 CTCACGTTCTTATCTTATGATGATCTGCTGACACGATACCTCATCTTCAAGTGC 360  
QY 385 AAAGCAAAAGTGAATCTACAGAAACTGCATGCTGTGCTGCACTGCTGCGATGTG 444  
Db 361 AAAGCAAAAGTGAATCTACAGAAACTGCATGCTGTGCTGCACTGCTGCGATGTG 420  
QY 445 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 504  
Db 421 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
QY 505 TACATAGGAGACATGTTTAAATTTCAAAAGCTGCTTACATCATATGAAATTC 564  
Db 481 TACATAGGAGACATGTTTAAATTTCAAAAGCTGCTTACATCATATGAAATTC 540  
QY 565 ATCACTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624  
Db 541 ATCACTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
QY 625 GTCTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
Db 601 GTCTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
QY 685 TTCGGGCTCAGCGTGAATACTATTTTAAATGAGGGTCAATCCTGTTGTTTCTTCC 744  
Db 661 TTCGGGCTCAGCGTGAATACTATTTTAAATGAGGGTCAATCCTGTTGTTTCTTCC 720  
QY 745 TACCAATCTTTAAGATCTATTAATGATGATGATGATGATGATGATGATGATGATG 804  
Db 721 TACCAATCTTTAAGATCTATTAATGATGATGATGATGATGATGATGATGATGATG 780  
QY 805 AAGTTGCAATTTTAAACGAAATCTTGAAGTGAACAGCAATTAGCTGATGATTTG 864  
Db 781 AAGTTGCAATTTTAAACGAAATCTTGAAGTGAACAGCAATTAGCTGATGATTTG 840  
QY 865 CTCTCTTTGCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATGCTTATGCAAT 924  
Db 841 CTCTCTTTGCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATGCTTATGCAAT 900  
QY 925 TGTGTTTGTGCGGT 939  
Db 901 TGTGTTTGTGCGGT 915

RESULT 14  
ADO28919  
ID ADO28919 standard; cDNA; 918 BP.  
XX  
AC ADO28919;  
XX

Query Match 97.3%; Score 913.4; DB 8; Length 918;  
Best Local Similarity 99.9%; Pred. No. 1.9e-260;



Db 901 TGTGTTTGTCGGT 915

## RESULT 15

ID AAL57070 standard; DNA; 1040 BP.

AC AAL57070;

DT 17-SEP-2003 (first entry)

Human G-protein coupled receptor GAVEL8 DNA sequence.

KM Human protein coupled receptor; GAVR18; signal transduction;  
KM inflammation; physiological immunological response; antiinflammatory;  
KM antiaesthetic; antirheumatic; antiarthritic; antitense therapy;  
KM chromosomal mapping; tissue typing; forensic biology;  
KM predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;  
KM rheumatoid arthritis; gene; ds.

**OS Homo sapiens.**

	Key	Location/Qualifiers
FH		
FT		
CDS		1. .918

```
FT
/product= "GAVE18 protein"
```

PN WO2003042395

PD 22-MAY-2003.

08-NOV-2002; 2002WO-US035887.

PR 13-NOV-2001; 2001US-0354150P.  
DE 33-MAY-2003; 2003CT-000000001

XX  
DA /AVET ) AVENTIS PHARM INC

XX	Eishindred]o H	Cai J	Busch ST	Gassnerhuber T
PT				

WPI: 2003-457496/43.

F-100B, 4402/203-  
 XX  
 XX

PT New GAVEL8 polypeptide and nucleic acid molecule encoding the  
PT polypeptide, useful for preventing and treating a disease or disorder  
PT associated with aberrant expression or activity of GAVEL8, e.g. asthma or  
PT rheumatoid arthritis.

PS Claim 1; Fig 5; 88pp; English

This invention relates to a novel G-protein coupled receptor (GAVE18) that is involved in signal transduction in respect to inflammation and the physiological immunological response. Molecules which may modulate the signalling activity or signal transduction of the receptor may be anti-inflammatory, antiallergic, antirheumatic or antiarthritic. The GAVE18 receptor and the DNA sequence encoding it may be a target for antiallergic therapy or gene therapy. The nucleic acid molecule, GAVE18 proteins and antibodies may be useful in screening assays, detection assays (for example chromosomal mapping, tissue typing or forensic biology), or predictive medicine (for example diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics. The nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse agonist and antagonist are also useful for preventing or treating a disease or disorder associated with aberrant expression or activity of GAVE18, such as inflammation and immunological-related diseases or disorders, for example asthma, chronic obstructive pulmonary disease or rheumatoid arthritis. The present sequence is the DNA sequence encoding the GAVE18 protein of the invention

**SQ** Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;

Query Match	97.3%;	Score 913.4;	DB 9;	Length 1040;
Best Local Similarity	99.9%;	Pred. No. 2e-260;		

Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	25	ATGCTGGGCAAAATACCTCCAGAAATTCCTCTGGAAATCCATATGTGACACCCCACTTA	84
Db	1	ATGCTGGGCAAAATACCTCCAGAAATTCCTCTGGAAATCCATATGTGACACCCCACTTA	60
Qy	85	ATCAGCCTCACTTCATATAGTGTATATGGCGGGCTGTGGGTGTCAATTCATTCTTTTC	14
Db	61	ATCAGCCTCACTTCATATAGTGTATATGGCGGGCTGTGGGTGTCAATTCATTCTTTTC	12
Qy	145	CTCTCTGTGAAATAATGAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATTGGTGGTG	20
Db	121	CTCTCTGTGAAATAATGAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATTGGTGGTG	18
Qy	205	GTCACAGAGGTTTTCTGCTGA CAGGCCATTGGCTTGACCTCACTCATCAAGAAAGCT	26
Db	181	GTCACAGAGGTTTTCTGCTGA CAGGCCATTGGCTTGACCTCACTCATCAAGAAAGCT	24
Qy	265	TGAGATGTTGGGCTGCCCTTCGCAAAATTGTGAGTGCATGCTGCACATCCAGATGAC	32
Db	241	TGAGATGTTGGGCTGCCCTTCGCAAAATTGTGAGTGCATGCTGCACATCCAGATGAC	30
Qy	325	CTCAGCTTCCTATTCATATGTGTGATCCTGGTACCAAGATCACTCATCTTCTTCAAGTGC	38
Db	301	CTCAGCTTCCTATTCATATGTGTGATCCTGGTACCAAGATCACTCATCTTCTTCAAGTGC	36
Qy	385	AAAGAAAGTGGAAATTCACAGAAACCTGCATGCTGTGGCTGCCAGTGGCTGGCATGTGG	44
Db	361	AAAGAAAGTGGAAATTCACAGAAACCTGCATGCTGTGGCTGCCAGTGGCTGGCATGTGG	42
Qy	445	ACGCTGGTATGTCTATGTGGTACCCCTGGTGTCTCCGGTATGGAATCATGAGGAA	50
Db	421	ACGCTGGTATGTCTATGTGGTACCCCTGGTGTCTCCGGTATGGAATCATGAGGAA	48
Qy	505	TACAAATGAGAGCACTGTTTTAAATTTCA CAAAGAAGCTTGCTTACACATATGTGAAATC	56
Db	481	TACAAATGAGAGCACTGTTTTAAATTTCA CAAAGAAGCTTGCTTACACATATGTGAAATC	54
Qy	565	ATCAATATATATATATGATCTATTTTGTCAATGCGCTGTCTGTGATCTGTGGTCTTCCAG	62
Db	541	ATCAATATATATATATGATCTATTTTGTCAATGCGCTGTGTGATCTGTGGTCTTCCAG	60
Qy	625	GTCCTCATCATATATGTGATGAGTGGAGAGCTACGCACTCTTATCTATCCACAGAG	68
Db	601	GTCCTCATCATATATGTGATGAGTGGAGAGCTACGCACTCTTATCTATCCACAGAG	66
Qy	685	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTCACTCTGTGTTGTCTCTCC	74
Db	661	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTCACTCTGTGTTGTCTCTCC	72
Qy	745	TACCAATTTTATAGATCTATTACTTGAATGTGTGACGCAITTCGAATGCTGTAGCAGC	80
Db	721	TACCAATTTTATAGATCTATTACTTGAATGTGTGACGCAITTCGAATGCTGTAGCAGC	78
Qy	805	AAGGTTGACATTTATAGAAATCTCTTGAAGTGAACAGAAATTAGCGTCAATGATTTG	86
Db	781	AAGGTTGACATTTATAGAAATCTCTTGAAGTGAACAGAAATTAGCGTCAATGATTTG	84
Qy	865	CTTCTCTTTGTCTTTGGGGAGAGCAATGTTGTTAAGCAAAAGATATATGGCTTATGAAAT	92
Db	841	CTTCTCTTTGTCTTTGGGGAGAGCAATGTTGTTAAGCAAAAGATATATGGCTTATGAAAT	90
Qy	925	TGTGTTTGTGTCGT 939	
Db	901	TGTGTTTGTGTCGT 915	

Search completed: September 10, 2005, 04:04:52  
Job time : 550.362 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 01:56:38 ; Search time 3394.79 Seconds  
(without alignments)  
10528.586 Million cell updates/sec

Title: US-10-085-233B-3

Perfect score: 939  
Sequence: 1 atcgcaaaatgctgacttccc.....ggaatgctgttctgtgcgcg 939

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hnc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gest1: \*  
9: gb\_gest2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678.8	72.3	694	7	CO918710 AGENCOURT
2	588.2	62.6	717	7	CO918845 AGENCOURT
3	537.4	57.2	684	9	AG145972 Pan trogl
4	415.8	44.3	772	2	BF160725 601769127
5	346.8	36.9	580	8	A2554824 RPCI-23-2
6	338	36.0	455	8	AQ888495 HS_3162_B
7	325.8	34.7	678	5	BK952455 DKFZP/8IN
8	237.2	25.3	646	5	BG862323 602796201
9	203	21.6	499	6	CD699779 EST16303
10	181	19.3	649	4	BG461295 RST44080
11	162	17.3	283	4	BG221739 RST41554
12	146.8	15.6	478	4	BG145683 mac33c07.
13	146.2	15.6	2774	3	AK041317 Mus muscu
14	142	15.1	834	6	AJ455645 AJ455645
15	111	11.8	680	1	CA355790 627748 NC
16	86.4	9.2	661	6	BY748361 BY748361
17	82	8.7	705	7	CN793065 4128026 B
18	76.2	8.1	679	6	CD469227 Leuko52.2
19	72.2	7.7	733	6	CA050323 88a1x9b52
20	71.4	7.6	648	6	CB514250 88a1x9b54
21	70	7.5	659	9	BQ563030 H4079D04-
22	69.8	7.4	879	9	AY410745 Homo sapi
23	69.4	7.4	866	6	CD246184 AGENCOURT
24	69.4	7.4	866	6	CD246184 AGENCOURT

25	69.4	7.4	980	4	BM543468
26	68.6	7.3	542	6	CA965628
27	67	7.1	672	7	CO957761 AGENCOURT
28	64.4	6.9	671	6	BY752012
29	62.6	6.7	353	5	BY183952
30	61.2	6.5	679	6	BY750559
31	60.2	6.4	785	4	BI754749
32	60	6.4	450	6	CA576592
33	60	6.4	607	2	BB634972
34	60	6.4	689	6	BY751880
35	59.8	6.4	2919	3	AK038620 Mus muscu
36	59.8	6.4	2959	3	AK079529 Mus muscu
37	59	6.3	695	6	BY751732
38	58	6.2	718	7	CO570572
39	58	6.2	791	6	CD559646
40	58	6.2	791	6	CD559647
41	58	6.2	792	6	CD559648
42	57.6	6.1	631	6	CB476420 jn811BF01
43	57	6.1	895	6	CB565888
44	55.8	5.9	653	2	BB636445
45	55.6	5.9	730	7	CF147825

#### ALIGNMENTS

RESULT 1  
CO918710  
LOCUS  
AGENCOURT 30488597 NIH MGC 145 Homo sapiens CDNA clone  
DEFINITION  
IMAGE:7211820 5', mRNA sequence.  
ACCESSION  
CO918710.1 GI:51266406  
VERSION  
EST.  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
AUTHORS  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: IRB15 row: c column: 10  
High quality sequence stop: 489.  
Location/Qualifiers  
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/lab host="DH10B"  
/clone.lib="NIH MGC 145"  
/note="Vector: pCDNA3.1. Site 1: varies by clone. Site 2:  
varies by clone. ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XbaI/NotI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.presv.dat





OY	877	TTTGGGGAAGCATTGGTTTAGCAAAAGAATTAATTCGCTTAGAATTCGTTTGCC	936
Db	129	TTTTGGGGAAGCATTGGTTTAGCAAAAGAATTAATTCGCTTAGAATTCGTTTGCC	70
OY	937	CCT 939	
Db	69	CGT 67	
RESULT 3			
AG145972			
LOCUS			
DEFINITION	AG145972	684 bp	DNA linear GSS 08-JAN-2001
ACCESSION	Pan troglodytes DNA, clone: RP43-007622.TU, genomic survey		
VERSION	sequence.		
KEYWORDS	AG145972		
SOURCE	AG145972.1 GI:16675650		
ORGANISM	GSS.		
REFERENCE	Pan troglodytes (chimpanzee)		
AUTHORS	Pan troglodytes		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.		
REFERENCE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,		
AUTHORS	Tozoki,Y., Watanabe,H. and Sakaki,Y.		
TITLE	BAC end sequences of library RPCI-43		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 684)		
TITLE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,		
JOURNAL	Tozoki,Y., Watanabe,H. and Sakaki,Y.		
AUTHORS	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical		
TITLE	and Chemical Research (RIKEN), Genomic Sciences Center (GSC);		
JOURNAL	1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
AUTHORS	(E-mail:chimpe@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,		
TITLE	Tel:81-45-503-9111, Fax:81-45-503-9170)		
JOURNAL	Clones are derived from the chimpanzee BAC library RPCI-43 This BAC		
AUTHORS	end was generated during the R&D process and may have higher chance		
TITLE	of clone tracking errors.		
JOURNAL	PRIMERS		
AUTHORS	Sequencing: TU		
TITLE	LIBRARY		
JOURNAL	Vector : PBACe3.6		
AUTHORS	R.Site 1 : ECORI		
TITLE	R.Site 2 : ECORI.		
JOURNAL	Location/Qualifiers		
AUTHORS	1..684		
TITLE	/organism="Pan troglodytes"		
JOURNAL	/mol_type="genomic DNA"		
AUTHORS	/db_xref="taxon:9598"		
TITLE	/clone="RP43-007622.TU"		
JOURNAL	/sex="male"		
AUTHORS	/cell_type="lymphocytes"		
TITLE	/clone_lib="Rpci-43 Chimpanzee Male BAC Library"		
COMMENT			
ORIGIN			
Query Match	57.2%	Score 537.4	DB 9; Length 684;
Best Local Similarity	98.0%	Pred. No. 1.5e-140;	
Matches 544;	Conservative 0;	Mismatches 11;	Indels 0; Gaps 0;
OY	385	AAAAGCAAAGTGTGATTTCTTACAGAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG	444
Db	10	AAAAAATCCGGGCTTTCTTACAGAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG	69
OY	445	ACGCTGTGATTTGTCAATTTGGTACCCTGGTGTGCTCCGGTATGGAATCATGAGGAA	504
Db	70	ACGCTGTGATTTGTCAATTTGGTACCCTGGTGTGCTCCGGTATGGAATCATGAGGAA	129
OY	505	TACAATGAGAGCACTGTTTTAAATTTACAAGAGCTTGCTTACATATGTGAAATC	564
Db	130	TACAATGAGAGCACTGTTTTAAATTTACAAGAGCTTGCTTACATATGTGAAATC	189
OY	565	ATCAACTATGATAGTCAATTTTGTCAATAGCCGTGCTGTGATTTCTTGGTCTTCAG	624

Db	130	ATCAACTATATGATATGATTCATTTTGTTCATACGCCGTGCTGTGAATTCGTGGTCTTCCAG	249
Qy	625	GTCTTCATCATTAATGTTAGTGTGCAGAAAGCTACGCCACTCTTACTATCCACACAGAG	684
Db	250	GTCTTCATCATTAATGTTAGTGTGCAGAAAGCTACGCCACTCTTACTATCCACACAGAG	309
Qy	665	TTCTGGGCTCAGCTGAAAAACCTATATTTTATATAGGGGTCACTCTGTGTTTCTCTCC	744
Db	310	TTCTGGGCTCAGCTGAAAAACCTATATTTTATATAGGGGTCACTCTGTGTTTCTCTCC	369
Qy	745	TACAGATCTTAGGATCTATCTACTGAATGTTGACGATTCGAAATGCCGTGAGACG	804
Db	370	TACAGATCTTAGGATCTATCTACTGAATGTTGACGATTCGAAATGCCGTGAGACG	429
Qy	805	AAGTTGATTTTAAAGAAATCTTCTGAGTGAACAGCAATTAAGCTGATGATTTG	864
Db	430	AAGTTGATTTTAAAGAAATCTTCTGAGTGAACAGCAATTAAGCTGATGATTTG	489
Qy	865	CTTCTCTTGTCTTGGGGGAGCCATTGTTTAAAGAAAGATTAATGCTTAATGAAT	924
Db	490	CTTCTCTTGTCTTGGGGGAGCCATTGTTTAAAGAAAGATTAATGCTTAATGAAT	549
Qy	925	TGTGTTTGTGCGGT 939	
Db	550	TGTGTTTGTGCGGT 564	
RESULT 4			
LOCUS	BF160725	772 bp	mRNA linear EST 30-OCT-2000
DEFINITION	601769127P1 NCI CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',		
ACCESSION	BF160725		
VERSION	BF160725.1	GI:11040832	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 772)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbsi@mail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.jnl.gov		
	plate: LRAM9196 row: f column: 07		
	High quality sequence stop: 634.		
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	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="CZECH 11"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:3988230"		
	/tissue_type="spontaneous tumor, metastatic to mammary.		
	/stem_cell_origin="		
	/lab_host="DH10B"		
	/clone_11b="NCI_CGAP_Lu29"		
	/note="Organ: lung; Vector: pCMV-Sport5; Site_1: SalI;		
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.		
	library constructed by life technologies. Investigator		
	providing samples: Gilbert Smith, NIH"		
ORIGIN			
Query Match	44.3%	Score 415.8	DB 2; Length 772;
Best Local Similarity	79.2%	Pred. No. 4.2e-106;	



LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
AO888495	456 bp DNA linear	AO888495	1	GSS 10-NOV-1995									
HS_3162_B1_B01_MR_CIT	Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey sequence.	AO888495.1	GI:6344685										
		GSS.											
		Homo sapiens (human)											
		Homo sapiens											
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.											
		1 (bases 1 to 456)											
		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.											
		Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome											
		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)											
		99380589											
		10449764											
		Contact: Mahairas GG, Wallace JC, Hood L											
		High Throughput Sequencing Center											
		University of Washington											
		401 Queen Anne Avenue North, Seattle, WA 98109, USA											
		Tel: (206) 616-3618											
		Fax: (206) 616-3887											
		Email: jwallace@u.washington.edu											
		Clones may be purchased from Research Genetics (info@reagen.com).											
		BAC end Web Server: http://www.hbrc.washington.edu											
		Plate: 3162 Row: D Column: 1											
		Seq primer: M13 Reverse											
		Class: BAC ends											
		High quality sequence stop: 456.											
		Location/Qualifiers											
		1..456											
		/organism="Homo sapiens"											
		/mol_type="genomic DNA"											
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		/sex="male"											
		/clone_lib="CIT Approved Human Genomic Sperm Library D"											
		/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"											
ORIGIN													
Query Match	36.0%; Score 338; DB 8; Length 456;												
Best Local Similarity	97.3%; Pred. No. 3.6e-84;												
Matches 364; Conservative 0; Mismatches 7; Indels 3; Gaps 2;													
OY	403 TACAGAAAGTCAGTCTGTGGCTGGCCAGTGTGGCAGTGTGGAGCGTGGTGAATTCATT	462											
Db	1 TACGAAAGTCTGCTGCTGTGGCTGCCAGTGTGGCAGTGTGGAGCGTGGTGAATTCATT	60											
OY	463 GTGGTACCCCTGTGTCTCCCGGTATGAATCCATGAGAATCAATGAGACACTGT	522											
Db	61 GTGGTACCCCTGTGTCTCCCGGTATGAATCCATGAGAATCAATGAGACACTGT	120											

Db		301	AAACATATTTTTATGGGGTCACTCCTGTTTGTTT-CTTCCTACCAG--CTTAGAATC	357
Oy	763	TATTACTGAATGT	776	
Db		358	TATTACTGAATGT	371
RESULT 7				
BX952455				
DEFINITION	BX952455		678 bp mRNA linear EST 01-MAR-2004	
LOCUS	DKFZP781N17197.z1.781 (synonym: hlc4)		Homo sapiens cDNA clone	
VERSION	DKFZP781N17197.5,		mRNA sequence.	
KEYWORDS	BX952455.1		GI:43429371	
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 678)			
JOURNAL	Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., Osanger,A.,			
COMMENT	Fojo,G., Han,M. and Wiemann,S. EST (Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., et al.) Unpublished (2003) Contact: MIPS MIPS Ingelstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analyais, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; consortium of the German Genome Project. No sl sequence available. This clone (DKFZP781N17197) is available at the RZPD in Berlin, Please contact the RZPD: Resourcententrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers 1..678 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKFZP781N17197" /dev_stage="adult" /lab_host="DH10B" /clone_id="781 (synonym: hlc4)" /note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIB; cDNA-collection"			
FEATURES	source			
ORIGIN				
Query Match	34.7%;	Score 325.8;	DB 5;	Length 678;
Best Local Similarity	99.1%;	Pred. No. 1.2e-80;		
Matches 327;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Oy	7	AAATGTGACTTCCCAAGTAGCGCTGGCCACAATACTTCAGAAATCTCTTGGCATCT	66	
Db	349	ACAGGTACTTCCCAAGTAGCGCTGGCCACAATACTTCAGAAATCTCTTGGCATCT	408	
Oy	67	ATAATGACACCCCCTTAATAGCGCTCTACTTCAATAGTCTTAATGGCGGCTGGTGGT	126	
Db	409	ATAATGACACCCCCTTAATAGCGCTCTACTTCAATAGTCTTAATGGCGGCTGGTGGT	468	
Oy	127	GTCAATTCGATCTCTTTCCTCTGGTGAATAAGAACCCGGTAGAGTGCACACATGGCG	186	
Db	469	GTCAATTCGATCTCTTTCCTCTGGTGAATAAGAACCCGGTAGAGTGCACACATGGCG	528	
Oy	187	GTCAATTAAGTGTGTGTGCCACAGCGTTTTCTGTGTGACAGTGCATTTGCTTGACC	246	
Db	529	GTCAATTAAGTGTGTGTGCCACAGCGTTTTCTGTGTGACAGTGCATTTGCTTGACC	588	
Oy	247	TACCTCATCAAGAAGACTTGATGTTTGGGCTGGCCCTTCGCAATTTTGAATGCATG	306	
Db	589	TACCTCATCAAGAAGACTTGATGTTTGGGCTGGCCCTTCGCAATTTTGAATGCATG	648	

Qy 307 CTGCACATCCACATGTAAGCTTCACTGCTTCTTA 336  
|  
Db 649 CTGCACATCCACATGTAAGCTTCACTGCTTCTTA 678

RESULT 8  
LOCUS BG862323 646 bp mRNA linear EST 29-MAY-2001  
DEFINITION 602796201F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',  
mRNA sequence.  
ACCESSION BG862323  
VERSION BG862323.1 GI:14212861  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LHAM10828 row: b column: 01  
High quality sequence stop: 644.

FEATURES  
source  
1..646  
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/clone="IMAGE:4917024"  
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/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; Salt: Site\_2: Notti; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

ORIGIN  
Query Match 25.3%; Score 237.2; DB 4; Length 646;  
Best Local Similarity 79.4%; Pred. No. 1.4e-55;  
Matches 281; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 11 GTGACTCCGAAGTGGCTGGCCAGCAATTCCTGAGAAATTCCTGAGATCCATAG 70  
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Db 293 GTAAATGTTGAAGATGATGATATATATACCTTGAAATTCCTCTTGAGACCTATAC 352

Qy 71 TGAACCCCACTTAATCAGCCTCTACTCTCATAGTCTTAATGGCGGCTGTGGGTGTCA 130  
|  
Db 353 TGGCAGACCACTTAATCAGCCTCTACTCTCATAGTCTTAATGGCGGCTGTGGGTGTCA 412

Qy 131 TTTCATTTCTTTCTCTCTGCTGAAATGAACACCGGCTAGAGACCAATGGCGGTCA 190  
|  
Db 413 TCTCCATCCGCTCTCTCTGCTGAAATGAACACCACTTCAAGACCAATGGCGGTCA 472

Qy 191 TTAACTTGTTGGTGTGCACAGAGTTTTCGCGGAGAGGCAATTCGCTTGAACCTAC 250  
|  
Db 473 TCAACTCTGTGGTGTGCACAGAGTTTTCGCGGAGAGGCAATTCGCTTGAACCTAC 532

Qy 251 TCATCAAGAAGACTTGGATGTTGGGCTGCCCTTCTTCAAAATTTGATGATGCCATGCTGC 310

Db 533 TCATCAAGAAGACTTGGATGTTGGGCTGCCCTTCTTCAAAATTTGATGATGCCATGCTGC 592  
|  
Qy 311 ACATCCACATGTAAGCTTCACTGCTTCTTAATGATGATATCTCTGGACCAAT 364  
|  
Db 593 ATATCCACATGTAAGCTTCACTGCTTCTTCAATGATGATATCTCAATCATGAT 646

RESULT 9  
LOCUS CD699779 499 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST16303 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD699779  
VERSION CD699779.1 GI:32229387  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

FEATURES  
source  
1..499  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN  
Query Match 21.6%; Score 203; DB 6; Length 499;  
Best Local Similarity 100.0%; Pred. No. 6.1e-46;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GTGACTCCGAAGTGGCTGGCCAGCAATTCCTGAGAAATTCCTTGCATCTATAG 70  
|  
Db 297 GTGACTCCGAAGTGGCTGGCCAGCAATTCCTTGCATCTATAG 356

Qy 71 TGAACCCCACTTAATCAGCCTCTACTCTCATAGTCTTAATGGCGGCTGTGGGTGTCA 130  
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Db 357 TGAACCCCACTTAATCAGCCTCTACTCTCATAGTCTTAATGGCGGCTGTGGGTGTCA 416

Qy 131 TTTCATTTCTTTCTCTCTGCTGAAATGAACACCGGCTAGAGACCAATGGCGGTCA 190  
|  
Db 417 TTTCATTTCTTTCTCTCTGCTGAAATGAACACCGGCTAGAGACCAATGGCGGTCA 476

Qy 191 TTAACTTGTTGGTGTGCACAGC 213  
|  
Db 477 TTAACTTGTTGGTGTGCACAGC 499

RESULT 10  
LOCUS BG461295 649 bp mRNA linear EST 21-APR-2001  
DEFINITION RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG461295  
VERSION BG461295.1 GI:13749801  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL MEDLINE PUBLISHED	COMMENT	FEATURES
1 (bases 1 to 649)	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
1	Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElisalt, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kliska, A., Hese, J., Cothren, K., Lo, K., Offenbacher, J., Davis, J., and Ducar, M.	Creation of genome-wide protein expression libraries using random activation of gene expression	Nat. Biotechnol. 19 (5), 440-445 (2001)		
11329013					
11329013	Contact: Scott J. Cain				
3201 Carnegie Ave, Cleveland, OH 44115, USA					
Tel: 216 431 9900					
Fax: 216 361 9596					
Email: scain@atherys.com.					
location/Qualifiers					
1..649					
/organism="Homo sapiens"					
/mol_type="mRNA"					
/db_xref="taxon:9606"					
/cell_line="H1080"					
/clone_id="Atherys RAGE Library"					
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."					
ORIGIN					
Query Match	19.3%;	Score 181;	DB 4;	Length 649;	
Best Local Similarity	74.1%;	Pred. NO. 1.1e-39;			
Matches	355;	Conservative	0;	Mismatches	50;
				Indels	74;
				Gaps	7;
11	GTGACTTCCCAAGTATGCTGCGCCCAATACCTCCAGAAATTCCTTGCATCTATAG	70			
108	GTGACTTCCCAAGTATGCTGCGCCCAATACCTTCTTATCTATAG	151			
71	TGACACCCCACTTATGACGCTCTATCATATGCTTATGCGCGCTGATGGCTGCA	130			
152	TGACACCCCACTTATGACGCTCTATCATATGCTTATGCGCGCTGATGGCTGCA	211			
131	TTTCATTTCTTCTCTCTGCGGAAATGAACACCGGCTGACGACACATGGCGTCA	190			
212	TTTCATTTCTTCTCTCTGCGGAAATGAACACCGGCTGACGACACATGGCGTCA	254			
191	TTAACTTGGTGTGTCACAGCGTTTTTCTGCTGACAGTG-CCATTTGCTTACCTAC	249			
255	TTAACTTGGTGTGTCACAGCGTTTTTCTGCTGACAGTGCGCATTTTGGCTTACCTAC	314			
250	CTCATCAAGAAGACTTGATGTTTGGGCTGCGCTTCTGCAAAATTTGTGATGCTGCTG	309			
315	C-----CTTTGGGCTGCGCTTCTGCAAAATTTGTGATGCTGCTG	356			
310	CACATCCATGATGATCACTGCTGCTTCT-ATTCTATGTTGATGCTGCTGCTGCTGCTG	368			
357	AACATTCATGATGATCACTGCTGCTTCTTCTATGCGTATCTTCTGCGCGCGAT----	412			
369	CATCTCTTCAAGTCAAGCAAGCAAGTGAATTTCTACAGAAATTCATGCTGCTGCTGCTG	428			
413	-----CAAGCAAGCGGATCTT-TACAGAGTGTGCGCGCGCGCGGATGCTG	455			
429	CAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	487			
456	CAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	514			

DEFINITION	BS241554 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	R621739
VERSION	BG221739.1 GI:13747760
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 283) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
TITLE	
JOURNAL	
MEDLINE	21227151
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 233. Location/Qualifiers 1..283 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_id="Athersys RAGE Library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
FEATURES	
source	
Query Match	17.3%; Score 162; DB 4; Length 283;
Best Local Similarity	100.0%; Pred. No. 2e-34;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	11 GTGACTCCCAAGATGCTGGACCACATACCTTCAGAAATTCCTTGGATCCTTAG 70 
Db	122 GTGACTCCCAAGATGCTGGACCACATACCTTCAGAAATTCCTTGGATCCTTAG 181 
OY	71 TGACACCCCACTTATCAGCCTCTACTTCAATAGTGCTTATTGGCGGGCTGTGGTGA 130 
Db	182 TGAACCCCACTTATCAGCCTCTACTTCAATAGTGCTTATTGGCGGGCTGTGGTGA 241 
OY	131 TTTCATTTCTTTCTCTCTGTGTAATAAGAACCCTGTAG 172 
Db	242 TTTCATTTCTTTCTCTCTGTGTAATAAGAACCCTGTAG 283 
RESULT 12	
LOCUS	BGI45683 478 bp mRNA linear EST 01-FEB-2001
DEFINITION	mcc3c07.y1 Soares mouse 3NbMs Mus musculus cDNA clone
ACCESSION	BGI45683
VERSION	BGI45683.1 GI:12649019
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 478) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AUTHORS	
TITLE	



JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:1499380

Seq primer: -40RP from Gibco  
High quality sequence stop: 392.

## FEATURES

## Source

Location/Qualifiers

1. 478  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4001652"  
/sex="male"  
/tissue\_type="Spleen"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse 3NbWS"  
/note="Vector: pT713D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5].  
TGTACCAATCTGAAGTGGAGCGCGCTGTTTGTCTTTTGTCTTTTGTCTTTT  
3); double-stranded cDNA was ligated to Eco RI adaptor  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT713 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through  
three rounds of normalization, and was constructed by  
Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 15.6%; Score 146.8; DB 4; Length 478;  
Best Local Similarity 81.0%; Pred. No. 4.9e-30;  
Matches 183; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

714 TATAGGGGATCATCTGTTGTTGTTCCCTACCAAGTCTTAGATCTATTACTTGA 773  
1 TATAGGATCATCTATTATTGTTT-CTTCCCTACCAAGTCTTAGATCTATTACTTGA 59  
774 TGTGTGAGCATTTCGAATGCTGTAGCAGCAAGTTCATTTTAAACGAATCTTCTT 833  
60 TGTGTGAGCATTTCGAATGCTGTAAACGAAGTTCATTTTAAACGAATCTTCTT 119  
834 GAGGTGAACGCAATTGCTGCTATGATTTGCTTCTTGTCTTTGGGGAAGCCATTG 893  
120 GAGCAACAACGCCATCGCTGCTGTGATTTGCTGCTTTTGTCTTGGAGGAAGCCATTG 179  
894 GTTTAAGCAAAAGATAATGGCTTATGAATGTTGTTGGCCGT 939  
180 GGTTAACGAAGATTGTCACATGTAATGCTCTTATGCCAT 225

## RESULT 13

## AK041317

## LOCUS

AK041317 2774 bp mRNA linear HTC 03-Apr-2004

## DEFINITION

Mus musculus adult male aorta and vein cDNA, RIKEN full-length  
enriched library, clone:A530099J19 product:hypothetical

Rhodopsin-like GPCR superfamily containing protein, full insert  
sequence.

## ACCESSION

## AK041317

AK041317.1 GI:26334372

## VERSION

HTC; CAP trapper.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Murinae; Mus.

## REFERENCE

## 1

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253

## PUBMED

## AUTHORS

10349636  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)

## JOURNAL

## MEDLINE

20499374

## PUBMED

11042159

## REFERENCE

## AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Komano, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishimura, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

## JOURNAL

20510913

## MEDLINE

11076861

## PUBMED

11076861

## REFERENCE

## AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

## JOURNAL

5

## REFERENCE

## AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## JOURNAL

5

## REFERENCE

## AUTHORS

6 (bases 1 to 2774)  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komano, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnara, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

## TITLE

## JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-32 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-ressgsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

URL: http://genome.gsc.riken.jp/  
URL: http://phantom.gsc.riken.jp/.  
URL: http://genome.gsc.riken.jp/.

## FEATURES

## Source

1. 2774  
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/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="PANTOM DB:A530099J19"  
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/clone="A530099J19"  
/sex="male"  
/tissue\_type="aorta and vein"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"



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/db_xref="GI:26334373"
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VSGVILGHMYLFLIPLVAILVRLILYFKLQOQOLQKRAVALSLIIWVGSEIPLP
IPLQVGTDPSTYEOQCEFEHKSINSRDIILINYSIIIVMTTLLFLILQAVILH
LIRAYMDMAHOEYRAOIKSFPEFLIVIVCFIPIHAFRVYFIQNPFEQNSDLILYN
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ORIGIN
Query Match 15.6%; Score 146.2; DB 3; Length 2774;
Best Local Similarity 51.7%; Pred. No. 1.5e-29;
Matches 412; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

QY 101 TAATGCTATTGGGGGCTGGTGGTCTCATTTTCATTTCTTCTCTGGTGAATAAATGA 160
DB 423 TGGTCTTCTTGGAGGACCGGTGGAAAGATTATGATGTCAACATGATGTCAAGAGA 482
QY 161 ACAACCGGTCAGTACACCAACGCGGTCACTTAAGTGGTGGTGCACAGGCTTTTC 220
DB 483 ATTGCCAATCAAGATTCCTCATCTATCATTTATCATTTGTTGCTCCCTTCTCC 542
QY 221 TGCTGACGTGCATTTGCTTGCCTGACCTCATCTCAAGAAAGACTTGATTTGGCTGC 280
DB 543 TGATTAGTGCATTCGCGCTCAGTTACTATTTCTCAGCAGTCTGGAACCTTGGCTT 602
QY 281 CTTTTCGAATTTTGAATGTCATGTCGACATCCACATGATCTCAAGTCTTCTTCT 340
DB 603 TTAACCTGCCAAGTGTAGTGGCTCATATATGTCATATGATCACTTCACTTCAATTTT 662
QY 341 ATGAGTGATCCGGTACACAGATACCTCATCTTCTCAAGTCAAGAAAGATGGAAT 400
DB 663 ATGTGGCATTTGTACCTTGGCTGCTCATCTATTTTAAG---AAATCGAAATGCAAC 719
QY 401 TCTACAGAAAATGTCATGTCGTGGCTGCAGTGTGCATGTCGACGCTGGTATTTCA 460
DB 720 AGTTACAAAAGTTCAGTGGCGGTGCTAGTATTTATTTGGGTGACAGAAAGCTTCA 779
QY 461 TTGTGTATCCCTGGTGTCTCCCGGTATGAAATCCATGAGAAATACATGAGAGAC- 519
DB 780 TCTTTTACCAATATTTTTCACAAATATGSCACAGATCCAAAGTTATACAGACAAAGC 839
QY 520 --TGTTTAAATTTCAAGAGCTTGTCTTACATATGGAATGGAATCATCATATGA 577
DB 840 GGTGCTTGAATTCATTAATCTCTCAATCCAGGACATCATCATTAATCATTTCTA 899
QY 578 TAGTCAATTTTGTATAGCCGTGTGTGTGATTTGTTGTCTTCCATGCTTTCATCA 637
DB 900 TAATGTATATGATGACAAAGTCTGTCTCTTCTTGTATGATGATGCTGTCTATTC 959
QY 638 TGTGATGTGCAAGAGTACGCCACTTTTACTATCCACAGAGTTCTGGGCTCAGC 697
DB 960 TTCAATTTGATAAAGCTTATGACCTGATATGAGGCGCCATCAAGAGTACAGAGCTCAA 1019
QY 698 TGAATAACCTATTTTATAGGGGTATCTTGTGTGTCTTCCCTACCAATCTTTTA 757
DB 1020 TCAAGAGTTTTCCTCTGTTGTGTATGATGTGTCTTATTAACCCACATGCAATCA 1079
QY 758 GATCTATTTATGATGATGTGACGCAATTCATGCTGTAGCAGCAAGTGTGCAATTT 817
DB 1080 GGGTATATTTTATTCAAAATTTTCCAGAGCAAGAAATTTCT-----AACTTAATCTGT 1133
QY 818 ATTAAGAAATCTTCTTGAAGTGAACAGCAATGATGCTGATGATTTGCTTCTTGTCT 877
DB 1134 ACAATGAATCTGTGTGTGTTAAAGCTTTCTGCTGCTGATGATGTTATGTTTCAATAG 1193
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QY 878 TTGGGGGAAGCCATTGG 894
DB 1194 GTGTGTCAATTCATTAG 1210

RESULT 14
AJ455645 834 bp mRNA linear EST 22-APR-2002
AJ455645 riken1 Gallus gallus CDNA clone 6b4r1, mRNA sequence.
AJ455645
AJ455645
VERSION AJ455645.1 GI:20265741
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Bukarya; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 834)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
CONTACT: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1..834
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="6b4r1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
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/notes="CB inbred strain"

ORIGIN
Query Match 15.1%; Score 142; DB 1; Length 834;
Best Local Similarity 64.1%; Pred. No. 1.4e-28;
Matches 225; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

QY 81 CTAAACACGCTCTACTTATGATGCTTATTTGGCGGCGTGGTGGTCAATTTCAATTC 140
DB 438 CTGATTAATCTGTACTCAATGCTCTTGTGAGGTGGATGATGCACTGCAATGTC 497
QY 141 TTTCCTCTGTGGAATGAAACACCGGTCAAGTACCAACATGCGGTATTAATTTGAT 200
DB 498 ATTGTGCTGTGCAAGATGAAAGTGTGTGTGTGACCACTACAGCATTAATTAATGAT 557
QY 201 GGTGTGTCACAGGCTTTTCTGTGACAGTGCATTTGCTTGAATCTTCAATCAAGAA 260
DB 558 TGTGTGATCAATGCTCTCTTCTCTCAAGTGCCTTCCGTGCACTATATGTCATTA 617
QY 261 GACTTGATGTTGGCTGCGCTTCTGCAATTTGTGATGTCAGTGCATGATCCACAT 320
DB 618 GAGTGTATCTTCCACATACATTCATTAATGAGTGTATGATGTCACATCCACAT 677
QY 321 GTAATCAAGTCTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 379
DB 678 GATATTTGATCTTCTTATTTTATGATGATGATGATGATGATGATGATGATGATGATG 737
QY 380 AGTCAAGAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCA 430
DB 738 AATGGAAGACANAGTGAAGTTTATAGAAAGCTTCATGCAATGCTTCA 788

RESULT 15
CA355790 680 bp mRNA linear EST 05-NOV-2002
CA355790 627748 NCCMA 1RT Oncohynechus myiiss CDNA clone 1RT8K09_A_F05 5',
ACCESSION CA355790
mRNA sequence.
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VERSION CA355790.1 GI:24600977  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)  
ORGANISM Oncorhynchus mykiss  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 680)  
AUTHORS Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,  
Koop, B., Gahr, S.A., Palci, Y. and Quackenbush, J.  
TITLE Sequence analysis of a rainbow trout cDNA library and creation of a  
gene index  
JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)  
COMMENT Contact: Rexroad CE  
USDA, ARS, National Center for Cool and Cold Water Aquaculture  
11876 Leetown Road, Kearneysville, WV 25430, USA  
Tel: 304 724 8340 x2129  
Fax: 304 725 0351  
Email: crexroad@nccwa.ars.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified by  
cross match v0.990329.  
Seq primer: AGCGATTAACAATTTCACACAGGA.  
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library made from pooled tissue from brain, gill, liver,  
spleen, muscle, and kidney."

ORIGIN

Query Match 11.8%; Score 111; DB 6; Length 680;  
Best Local Similarity 55.9%; Pred. No. 7.7e-20;  
Matches 210; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 134 CCATTCCTTTCTCTCTGTAAGAAATGAACACCGGTCACTGACACCATGCGGTCAATTA 193  
DB 305 CCTGATGATGCACATCTCCATCCACATGATGATCACTTATCACATGCGTATGCTCA 364  
QY 194 ACTTGGTGTGTCCACAGCGTTTTCCTGACAGTGCATTTGGCTTGAAGCTTCACTCA 253  
DB 365 ACCCTACCGTGGCCCACTTCCTGTTCTACTCACCGTACCGTTCAGAGATCTACTATG 424  
QY 254 TCAAGAACTTGGATGTTGGGCTGCGCTTTCGCAATTTTGTGAGTGCATGTCACCA 313  
DB 425 CTGCTGTACTGATGTTGGGGAGATGCTGTGAGGAGTCACTGTCATGATCCACG 484  
QY 314 TCCACATGTAAGTCAAGTTCATTTCTATGTTGATGCTGCTGTCACAGATACCTCATCT 373  
DB 485 TGCACATGTAAGTGGCTTTGTTTCTAGTGGTCACTCTGTCATAGCATGCTGGGGT 544  
QY 374 TCTTCAAGTCAAGAAAGTGAATTTTACAGAAAACTGCATGCTGTGGCTGCCAGTG 433  
DB 545 TCCATAGCAAGAGATTCCTACGATTTTACAGGAAGTTGATGCTTTTGGCGCCAGTG 604  
QY 434 CTGGCATGTGACGCTGTGATTTGTCAATGTGTGTAACCGGTGTTCTCCCGTATAGAA 493  
DB 605 TGGCAGTGTGACAGTATGCTTATGATCATCCCCCATCTTATTACAACTACGGCA 664  
QY 494 TCCATGAGGATACAA 509  
DB 665 AGGACGTCCAGATAA 680



Db 499 GCCCAGGCTGTGCATGTGGCCATCTGTGGCCCTGTGTCGTTGCCGTTGCC 558  
Qy 478 GTCTCCCGGTATGGAATCCATGAGGAATCAATGAGAGACATGTTTAAATTGCAAA 537  
Db 559 ATATGAGGCTCGGCACAGCTGCGAGATGAAGATGATGATGCTGGTGAGATCCCTACC 618  
Qy 538 GAGCTTGCTTACACATATGTGAATAATCATCACTATATATGATGATGATTTTGTATAGCC 597  
Db 619 CCGCAGGATTAACGAGGAGCCCGGAGTTTGCCATCTGCATCTCTCTCTCTCTCATGTC 678  
Qy 598 GTTGTGTGATCTGTGTGTTGTTCCAGGCTTCAAT 635  
Db 679 CCCGTCTGTGCATCTGTGTCTGTACAGCTCATGAT 716

RESULT 2  
US-08-405-271A-18  
Sequence 18, Application US/08405271A  
Patent No. 6432652  
GENERAL INFORMATION:  
APPLICANT: EVANS, CHRISTOPHER J.  
ATTORNEY/AGENT INFORMATION:  
KEITH, DUANE E.  
TITLE OF INVENTION: OPIOID RECEPTOR GENES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405,271A  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20526.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1805 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..1119  
US-08-405-271A-18

Query Match 8.1%; Score 76.4; DB 3; Length 1805;  
Best Local Similarity 46.7%; Pred. No. 1.5e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy 118 CTGGTGGGTGTCATTTCCATCTTTCTCTCTGTGAAATGAACCCGGTCAAGTACC 177  
Db 208 CTGGGGAACCTGCTTTCATGATGATCTTCAAGCACCAAAATGAAGACAGCCACC 267  
Qy 178 ACCATGGCGGTCAATTAATCTGTGTGTGTCACAGCGTTTTCGTGACAGTCCATT 237  
Db 268 AATATTTAATCTTTAACTCGGCGCCGACACATCTGTCTGTGACGCTGCCCTTC 327  
Qy 238 CGCTTGAACCTCACTCAAGAAAGACTTGATGTTGGGCTGCCCTTCTGCAAAATTGTG 297

Db 328 CAGGCAACGACATCTCTCTGGCTTCTGCGCGTTGGGAATGCCCTGTGCAAGACAGTC 387  
Qy 298 AATGCAATCTGACATCAATCAATGATCACTCAAGTTCCATTTATGTGTATCTGTGTC 357  
Db 388 ATTGCCATGATCTACTCAACAATGTTCAACAGCACCCTTCACTTAAGTCCATGAGTGTG 447  
Qy 358 ACCAGATACCTCATCTTCTTCAAGTGAAGAAAGCAAAAGTGAATTTACAGAAATGTCAT 417  
Db 448 GATGCGTATGATGACATCTGCCACCCCATCCGCGCTGTGAGTCCGACAGTCCAGCAA 507  
Qy 418 GCTGTGCTGCAAGTCTGACATGTGACGCTGTGATGATGATGATGATGATGATGATGAT 477  
Db 508 GCCCAGGCTGTCAATGTTGAGCCATCTGTGGCCCTGTGCTGTGCTGTGCTGTGCTGTG 567  
Qy 478 GTCTCCCGGTATGGAATCCATGAGGAATCAATGAGAGACATGTTTAAATTGCAAA 537  
Db 568 ATCATGAGGCTCGGCACAGGTGAGATGAAGATGATGATGATGATGATGATGATGATGAT 627  
Qy 538 GAGCTTGCTTACACATATGTGAATAATCATCACTATATGATGATGATGATGATGATGATG 597  
Db 628 CCTCAGGATTAACGAGGAGCCCGGAGTTTGCCATCTGCATCTCTCTCTCTCTCATGTC 687  
Qy 598 GTTGTGTGATCTGTGTGTTGTTCCAGGCTTCAAT 635  
Db 688 CCCGTCTGTGCATCTGTGTCTGTACAGCTCATGAT 725

RESULT 3  
US-09-016-434-1391  
Sequence 1391, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
ATTORNEY/AGENT INFORMATION:  
JEFFREY J. SEIDAMER  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1391:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1973 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK

CLONE: 9471316  
US-09-016-434-1391

Query Match 8.1%; Score 76.4; DB 4; Length 1973;  
Best Local Similarity 46.7%; Pred. No. 1.5e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

```
QY 118 CTGATGGGTGATTCATTCATCTTTCTCTGTTGAAAAGAACCCGGTACGTACC 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 CTGGGGAATGCTCTTGATGATGATGATCTTCAAGGACACCAAAAGAAAGACGAC 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 ACCATGCGGTGATTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 AATATTACATCTTTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 CGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 496 CAGGACACGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 AGTGCATGCTGACATCCACATGATCTACCTTCTATTTATGTTGATCTGTC 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 556 ATTGCATTTACATCTTACATCAATGTTACACGACCTTCACTTACCTTACCTTACCTT 615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 ACCAGATACCTCATCTTCTTCAAGTGCAAGAACAAAGTGAATCTACAGAAACTGCAT 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 616 GATGCTATGATGACATCTGACATCCCATCCGTCCTGACGTCGACGTCAGACAA 675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 676 GCCCAGGCTGTCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478 GTCTCCCGGTATGAAATCCATGAGATATACATGAGAGACATGTTTAAATTTACAAA 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 736 ATCATGGGCTTCGACAGTTCAGAGATGAAGATGAGCTGAGGATCCCTAAC 795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 538 GAGCTTGTACATCATATGTAATATCATATATGATGATGATGATGATGATGATGATGAT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 796 CCTCAGATTTACTGGGGCCCGGTGTTGCTGATCTGATCTTCTCTTCTCATGTC 855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 598 GTTGTCTGTATCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 856 CCCGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 4  
US-09-023-655-1417

; Sequence 1417, Application US/09023655  
; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/023,655

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1417:

SEQUENCE CHARACTERISTICS:

LENGTH: 1973 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9471316

US-09-023-655-1417

Query Match 8.1%; Score 76.4; DB 4; Length 1973;  
Best Local Similarity 46.7%; Pred. No. 1.5e-12;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

```
QY 118 CTGATGGGTGATTCATTCATCTTTCTCTGTTGAAAAGAACCCGGTACGTACC 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 CTGGGGAATGCTCTTGATGATGATGATCTTCAAGGACACCAAAAGAAAGACGAC 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 ACCATGCGGTGATTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 AATATTACATCTTTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 CGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 496 CAGGACACGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 AGTGCATGCTGACATCCACATGATCTACCTTCTATTTATGTTGATCTGTC 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 556 ATTGCATTTACATCTTACATCAATGTTACACGACCTTCACTTACCTTACCTTACCTT 615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 ACCAGATACCTCATCTTCTTCAAGTGCAAGAACAAAGTGAATCTACAGAAACTGCAT 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 616 GATGCTATGATGACATCTGACATCCCATCCGTCCTGACGTCGACGTCAGACAA 675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 676 GCCCAGGCTGTCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478 GTCTCCCGGTATGAAATCCATGAGATATACATGAGAGACATGTTTAAATTTACAAA 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 736 ATCATGGGCTTCGACAGTTCAGAGATGAAGATGAGCTGAGGATCCCTAAC 795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 538 GAGCTTGTACATCATATGTAATATCATATATGATGATGATGATGATGATGATGATGAT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 796 CCTCAGATTTACTGGGGCCCGGTGTTGCTGATCTGATCTTCTCTTCTCATGTC 855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 598 GTTGTCTGTATCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 856 CCCGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5  
US-09-976-594-171

; Sequence 171, Application US/09976594  
; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409



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Db 277 GCAACACCAAAATGAGACAGCCACCAATATTATCATCTTTAACTGGCCCTGCGCCGACAC 336
Qy 213 CGTTTTCGTGCTGACAGTGCATTTGGCTTGACCTCATCAAGAAAGCTTGAGATT 272
Db 337 TCTGCTCTCTGACGCTGCTCCCTTCAGGGCAGGACATCTCTGGGCTTCTGGCCGTT 336
Qy 273 TGGGCTGCGCTTCTGCAAAATTTGTAGTGCATCTGACATCCACATGATACCTCAGTT 332
Db 397 TGGGAATGCGCTGTCGAAGACAGTCATTTGACATTAACAAACATGTTACACGACAC 456
Qy 333 CCAATTATGATGTGATCTCTGTCACCAATACCTCATCTTTCAAGTGCAGAAACAA 332
Db 457 CTTACACCTTAATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
Qy 393 AGTGAATTCATACGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 452
Db 517 CTTGAGCTGCGACGCTGACGAAAGCCGAGCTGATGATGATGATGATGATGATGATGAT 576
Qy 453 GATTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 512
Db 577 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636
Qy 513 GAGACACTGTTTAAATTTCAAAAGCTTCTTACATATGTAAGAAATCAATCACTA 572
Db 637 CGAGTGCCTGATGAGATCCCTACCTCAGATTAATGAGGCGCCGCTGTTGCTGCTG 656
Qy 573 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
Db 697 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756
Qy 633 CAT 635
Db 757 GAT 759

```

## RESULT 8

US-09-910-695-9

```

; Sequence 9, Application US/09910695
; Patent No. 6737252

```

## GENERAL INFORMATION:

```

; APPLICANT: Hedrick, Joseph A.
; Vicari, Alain P.
; Zlocnik, Albert

```

```

; TITLE OF INVENTION: Mammalian Chemokines; Receptors;
; Reagents; Uses

```

```

; NUMBER OF SEQUENCES: 10

```

```

; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104

```

```

; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: Patentin Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/910,695

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```

; FILING DATE: 20-Jul-2001

```

```

; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 09/122,585

```

```

; FILING DATE: 24-Jul-1998

```

```

; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0757
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200

```

```

; INFORMATION FOR SEQ ID NO: 9:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 429..1238
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 60/053,693
; FILING DATE: 25-Jul-1997
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-910-695-9
Query Match 6.7%; Score 62.8; DB 4; Length 1273;
Best Local Similarity 45.7%; Pred. No. 1.6e-08;
Matches 255; Conservative 0; Mismatches 302; Indels 1; Gaps 1;

```

```

Qy 81 CTTAATCAGCTCTACTGATAGTGTATTGAGCGGGCTGAGGCTGATTTCCATTCT 140
Db 321 CTTAGCTTTTACAGCTGATCTTCTGATGAGGCTGTTTATGATCATGCTGCTTGG 380
Qy 141 TTCTCTCTGTAATAATGAAACACCGGTCAGTGAACCAATGCGCGTATTAACTTGGT 200
Db 381 GGTTCACAGTGAACCAAGAAAGAAACAG-TCACATCTCATATGATGACGTTGC 439
Qy 201 GGTGTCACAGGTTTTCTGCTGACAGTGCATTTGCTTGAACCTTACCTCATCAAGAA 260
Db 440 ACTACTGACCTGATTTTATTAATCTAGTCTGCCCTTGGAGTGTATTAATGCAAAAG 499
Qy 261 GACTTGATGTTTGGGCTGCCCTTTCGCAAAATTTGAGTGCATCTGCAATCCACAT 320
Db 500 CGAGTGCATTTGAGAGTACTTTCGCCAATTTCTGGGCGCTGAGTGTGTTTAAACC 559
Qy 321 GTACCTCAGCTTCATTTGATGAGTGTGATGATGATGATGATGATGATGATGATGAT 380
Db 560 AAGCTGCTCTGCTGCTGCTTCTTCTTCAATGATGATGATGATGATGATGATGATGAT 619
Qy 381 GTGCAAGACAAAGTGAATTTTCAAGAAATGCAATGCTGTGCTGCAAGTGTGGCAT 440
Db 620 GCCAAATATGCAAGAGAGCTGAAGAACCGGCAAGGCGTGTGCGGTGGGGGGG 679
Qy 441 GTGACGCTGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
Db 680 CTGGTGAATGACCTTACCAACCACTGCTCCCTGCTACTGCTTACGAAGACCCAGCAA 739
Qy 501 GGAATCATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACATATGATGAA 560
Db 740 TGCCTCTCCCGGCACTGCTGAGATCTCCGATCAACCACTTAAAGCTTCAA 799
Qy 561 AATCATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
Db 800 CGTCTCACTTCAAGCGACATATTTTCTTCCGATCCCTTGTTCATCATATGATCG 859
Qy 621 CCAAGCTTTCATCATATAT 638
Db 860 GTGCTACGTGTCATCAT 877

```

## RESULT 9

US-08-147-592A-5

```

; Sequence 5, Application US/08147592A
; Patent No. 6096513

```

## GENERAL INFORMATION:

```

; APPLICANT: Bell, Graeme I

```

```

; APPLICANT: Reisine, Terry

```

```

; TITLE OF INVENTION: Opioid Receptor Genes,
; Compositions and Methods

```

```

; NUMBER OF SEQUENCES: 43

```

```

; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: Arnold, White & Durkee

```



STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 72210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,592A  
FILING DATE: 05-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30-JUL-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 161..1261  
US-08-147-592A-5

Query Match 6.4%; Score 59.8; DB 3; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 1.4e-07;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

33 CCACATPACTCTCAGAGATTCCTTGGCATCTCTATAGTACACCCCATTTATACGCT 92  
262 CCTCAATGCTAGGACAGAGGCTTCTCCCTTGAGCTCAAGTCAACATCGGAGGCT 321  
93 CTAATTCATAGTCTTATTTGGCGGCTGGTGGG---TGTCAATTCATTTCTTCTCCT 149  
322 CTACTTGGCTGTGTGATCGGGGGGCTCCCGGGAATGCTGTGATGATGATCTATCT 381  
150 GGTGAAGAATGACACCCGGTCACTGACACCATGAGCGGCTATTAACTTGGTGGTCC 209  
382 CAGGACACACCAAGATGAAGACTGCTACCAATTTACATTTAACTGGCACTGGCTGA 441  
210 CAGCGTTTCTGCTGACATGACATTTGCTTGACCTTACCTCATGAAGAAGCTTGAT 269  
442 TACCTGGTCTTCTGACACTGCGCTTCCAGGGCAGAGAAATCTTCTGGGCTTGGCC 501  
270 GTTTGGGCTCCCTTCTGCAAAATTTGAGTGCATGCTGCACATGCACATGTAACCTCAC 329  
502 ATTGGGAATGACACTGTGCAAGACGCTCATTTGCTATCGACTATCAACAATGTTTACAG 561  
330 GTTCTATTCTATGTGTGATCTCTGTGACCAAGATACCTCATCTTCTTCAAGTCAAAGA 389  
562 CACTTTCATTTGACTGACATGAGTGAACCGTTAATGATGATCTGACCACTTATCCG 621  
390 CAAAGTGAATTTCAAGAAACTGCAATGCTGTGGCTGCAAGTCTGGCATGTGAGAGCT 449  
622 TGGCTTGATGTTGGAGCATCCAGTAAAGCCAGGCGCTTAAATGTGGCCATATGAGGCCCT 681

450 GGTGATTTGATTTGTGATACCCCTGGTGTCTCCCGTATGGAATTCATGAGAAATACAA 509  
682 GGCTTCGGTGTGTGGTGTCTCTGTGGCATCATGGAGCTCAGCAAGTGAAGATGAAGA 741  
510 TGAAGACACTGTTTAAATTTCAACAAGAGTTGCTTACACATATGGAATCATCA 569  
742 GATGAGTGCCTGGTGAAGATCCCGCCCTCAGACATTTGGGCGCTGATTTGGCCAT 801  
570 CTATATGATGATCATTTTGTGATGACCGTTCGTGATTTCTGTTGCTTCAGGTCCT 629  
802 CTGATCTTCTCTTTTCTTCTTCAATCATCCGCTTGTGATCATCTGTGTGCTACGCT 861  
630 CATCAT 636  
862 CATGATT 868

RESULT 10  
US-08-292-694A-5  
Sequence 5, Application US/08292694A  
Patent No. 6319666  
GENERAL INFORMATION:  
APPLICANT: BELL, GRAEME  
APPLICANT: REISINE, TERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,694A  
FILING DATE: August 19, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20 May 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 July, 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/147,592  
FILING DATE: 5 No. 6319666ember 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US94/05747  
FILING DATE: 20 May 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS

LOCATION: 161..1261  
US-08-292-694A-5

Query Match 6.4%; Score 59.8; DB 3; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 1.4e-07;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

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Qy 33 CCACATATCTCCAGAAATTCCTCTGGATCTTATGACACCCCACTTAATAGCCT 92
Db 262 CCTCATCTGATGACACAGTGCCTTCTGCTCCCTTGAATCAAGGTCACCATGTGGGCT 321
Qy 93 CTACTTCAATGCTTATTTGGCGGGCTGGTGG--TGTCAATTCATCTTTTCTCTCT 149
Db 322 CTACTTGGCTGTGTCATCGGGGGGCTCTGGGAACTGCTCGTCAATGATGATCTCT 381
Qy 150 GGTGAAATGAAACCCCGTCACTACCACTGCGGCTCATTAATTTGGTGTGTCCA 209
Db 382 CAGGACACCAAGAAAGACTGCTACCAACTTACATATTTAATTTGGACATGGCTGA 441
Qy 210 CAGGCTTTTCTGCTGACAGTGGCATTTGGCTGACCTACCTCAACAGAACTTGGAT 269
Db 442 TACCTGCTCTGCTGACATGCTCCCTTCAGGGACAGACATCTTCTGGGCTTCTGGCC 501
Qy 270 GTTTGGGCTGCTCTGCAATTTGTGAGTGCATGCTGCAATCCACATGATCTCAC 329
Db 502 ATTTGGGAATGACATGCTGCAAGAGCGTCAATGCTATGCACTACCAACATGTTTACAG 561
Qy 330 GTTCTTATTTCTATGTTGATGCTGCTGCAACAGATACCTCAATCTTTCAAGTGCMAA 389
Db 562 CACTTTCATTTGACTGCTGATGATGAGTACCGTTATGATGATCTCCACCTTATCG 621
Qy 390 CAAGTGAATTTACAGAAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
Db 622 TGCCCTGATGTTGGACATCAAGTAAAGCCAGGCGTTATGATGAGGCAATGAGGCTT 681
Qy 450 GGTGATGCTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
Db 682 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
Qy 510 TGAGAGACATGTTTAAATTTCAAAAGACTGCTTACATATGTAAGAAATCATCA 569
Db 742 GATGAGTGTGCTGATGAGATCCCGCCCTCAGGACTATGAGGCGCTGATTTGCTAT 801
Qy 570 CTATATGATGATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
Db 802 CTGATCTCTCTTTTCTTCTTATCATCCGCTTCTGATCATCTGCTGCTGCTGCTGCT 861
Qy 630 CATCAT 636
Db 862 CATGATT 868

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## RESULT 11

US-08-889-108-16  
Sequence 16, Application US/0889108  
Patent No. 6103492  
GENERAL INFORMATION:  
APPLICANT: Yu, Lei  
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/305,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
TELEPHONE/DOCKET INFORMATION:  
TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 173..1273  
US-08-889-108-16

Query Match 6.4%; Score 59.8; DB 3; Length 1567;  
Best Local Similarity 45.6%; Pred. No. 1.5e-07;  
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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Qy 89 GCTCTCATCTATGAGTCTTATTTGGGGGCTGGTGG--TGTCAATTCATCTTTTCC 145
Db 330 GGTCTATCTTGGCTGTGATGCTGAGGAGGCTCCCTGGGAACTGCTGCTGATGATGCA 389
Qy 146 TCTGTGAAATGAAACCCGCTCAGTGAACCACTAGCGGCTATTAATCTGCTGCTG 205
Db 390 TCTCAGAGACACCAATGAAAGCACTACCAATTTACATTTAATTTATGCTGCTG 449
Qy 206 TCCACAGCTTTTCTGCTGACAGTGCATTTGCTTGAACCTTACATCAAGAACTT 265
Db 450 CTGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
Qy 266 GATGTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
Db 510 GGCATTTGGGAATGCACTGCAAGACTGCTGATGCTGATGCTGATGCTGATGCTGAT 569
Qy 326 TCAAGTCTATCTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385
Db 570 CCAGCACTTTTATCTGACCGCATGAGCGTGAACCGCTATGCTGCTGCTGCTGCTGCT 629
Qy 386 AAGCAAAAGTGAATTTACAGAAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
Db 630 TCGTGCTTGAATGCTGACATCCAGAAAGCCAGGCTGTTAATGAGGCAATGAGG 689
Qy 446 CGCTGATGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 505
Db 690 CCTGCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
Qy 506 ACAATGAGAGCACTGTTTAAATTTCAAAAGACTGCTTACATATGTAAGAAATCA 565
Db 750 AAGAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
Qy 566 TCAATATATGATGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
Db 810 CCAATGCTATCTTCTTTTCTTATATATCCCTGCTGATCATCTGCTGCTGCTGCTGCT 869
Qy 626 TCTTCATCAT 636
Db 870 GCCTCATGATT 880

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## RESULT 12

PCT-US94-10358-16  
Sequence 16, Application PC/TUS9410358

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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDIA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 173..1273
; PCT-US94-10358-16

Query Match      6.4%; Score 59.8; DB 5; Length 1567;
Best Local Similarity 45.6%; Pred. No. 1.5e-07;
Matches 251; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

QY      89 GCCTCTACTTCAATGCTTATTTGGCGGCTGTGGG---TGTCATTTTCATTTCTTTCC 145
DB      330 GGCCTACTTGGCTGTGTGATGGGGGGCTCCCTGGGAACTGCTGTCATGTATGTCA 389
QY      146 TCCTGTGAAATGAACAACCCGGTCAGTGACCACTAGCGCGTCATTACTGGTGTGG 205
DB      390 TCCTCAGGACACCAAAATGAAGACAGCTACCAATTACATTTAATCTGGCACTGG 449
QY      206 TCACAGAGTTTCTGTCTGACAGTGCATTTGCTTGACCTTACTTCAAGAAAGCTT 265
DB      450 CTGTATACCTGTGTCTTGTCTAAGCTGCTTCCAGGACAGACATCTTACTGGGCTTCT 509
QY      266 GGAATGTTGGGCTCCCTTCTGCAAAATTTGAGTGCATGCTGCACATCCACATGTACC 325
DB      510 GGCATTTTGGGAAATGCACTCTGCAAGACTGTCACTTGTCTATGACTACCAACATGTTTA 569
QY      326 TCAGCTTCCTATTTCTATGTGTGTATCTGTGTACCAAGATACCTCATCTTTCAAGTGA 385
DB      570 CCACACACTTTTACTCTGACGCGCATGAGCGTATGCGTATGTGCTATGCGCACCTTA 629
QY      386 AAGCAAAAGTGAATTTCTACAGAAATGCAATGCTGTGGCTGCCAGTGTGGCATGTGGA 445
DB      630 TCCGTGCCCTTGATGTGTGAGCATCCAGCAAAAGCCAGGCTGTTAAATGTGGCCATATGGG 689
QY      446 CGCTGTGATTTGTATTTGTGTGTATCCCTGTGTGTCTCCGGTATGGAATCATGAGGAAT 505
DB      446 CGCTGTGATTTGTATTTGTGTGTATCCCTGTGTGTCTCCGGTATGGAATCATGAGGAAT 505
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DB      690 CCCTGGCTTCAGHGTGTGTGTTCTGTGGCATCATGAGTTCAGCAAGAATGAAGAT 749
QY      506 ACATATAGAGACACTGTTTAAATTTACAAAAGCTTGTCTTACATATGTGAAAATCA 555
DB      750 AAGAGATCAGATGCTGTGTGAGATCCGCCCTCAGAGACTATTTGGGGCCCTGTATTTG 809
QY      566 TCACTATATGATGATCATTTTGTGATAGCCGTTGCTGTGATTTCTGTTGTTCTTCAGG 625
DB      810 CCATCTGATCTTCTCTTTTCTTCTTATCATCCCTGTGTGATCATCTGTGTGCTACA 869
QY      626 TCTTCATCATTT 636
DB      870 GCCTCATGATT 880

RESULT 13
US-08-986-209A-1
; Sequence 1, Application US/08986209A
; Patent No. 6660496
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Pasternak, Gavril W
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTOR
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 830002-2004
; CURRENT APPLICATION NUMBER: US/08/986,209A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1402)
; OTHER INFORMATION:
US-08-986-209A-1

Query Match      6.4%; Score 59.8; DB 4; Length 2600;
Best Local Similarity 44.8%; Pred. No. 2.1e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

QY      33 CCACATATCTCCAGGAATTCCTTGGCATCTCTATATGACACCCCATTTATTCAGCCT 92
DB      400 CCTCAATGTCTAGGCAACAGTCCCTTCTGCCCCCTTGAGACTCAAGTCAACCATCGTGGGCT 459
QY      93 CTACTTCATATGCTTATTATGGCGGCTGGTGGG---TGTCATTTTCATTTCTTCTCTCT 149
DB      460 CTACTTGGCTGTGTGATCGGGGGGCTCTTGGGAACTGCTGTGATGTATGTATCTCT 519
QY      150 GGTGAAATGGAACACCCGGTCAGTGACCACTAGGCGGTCAATTAATCTTGTGTGTGCA 209
DB      520 CAGGACACACCAAGATGAAGCTGTACCAATTTACATTTAATCTGGCACTGGCTGA 579
QY      210 CAGCGTTTCTGTGTGACAGTGCATTTGCTTGACCTTACTATCAAGAAAGCTTGGAT 269
DB      580 TACCTGTGTCTGTGACACTGCTTCCAGGACAGACATCTTCTGTGGCTTCTGGCC 639
QY      270 GTTTGGGCTCCCTTCTGCAAAATTTGTAGTGCATGTCGACATCCACATGTAACCTCAC 329
DB      640 ATTTGGGAATGCACTGTGCAAGCGGCTATGTCTATGTACTTACCAACATGTTTACAG 659
QY      330 GTTCTATTTCTATGTGTGTATCTGTGTACCAAGATACCTCATCTTCTTCAAGTCAAGA 389
DB      700 CACTTTCATTTTACATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 759
QY      390 CAAAGTGAATTTCTACAGAAATGCAATGCTGTGGCTGCCAGTGTGGCATGTGAGAGCT 449
DB      760 TGCCTTTGATGTGTGACATCCAGTAAAGCCAGGCGCTTAAATGTGGCCATATGGGCGCT 819
QY      450 GGTGATTTGTATTTGTGTATCCCTGTGTGTCTCCGGTATGGAATCATGAGGAATCA 509
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Db	Qy	Db	Qy	Db	Qy
820	GGCTTCGGTGGTGGTGGTTCCTGTTGCCATCATGGGCTCAGCACAAGTGGAGGATGAGAGA	879			
510	TGAGGAGCACTGTTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATTCACAA	569			
880	GATCAGAGTCCCTGGTGGAGATCCCCGCCCTCAGACACTTTGGGGCCCTGTATTTGCCAT	939			
570	CTATATGATAGTCATTTTGTGCATAGCCGTGCTGTGATCTTGTTGGTCTTCAGAGCTT	629			
940	CTGCATCTTCCTTTTTCCTTCAATCATCCCGGTTCTGATCATCTCTGTCTGACAGCCT	999			
630	CATCATTT	636			
1000	CATGATTT	1006			

RESULT 14  
 US-08-454-549-1  
 : Sequence 1, Application US/08454549  
 : Patent No. 5866324  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: EPPLE, C. Mark  
 : APPLICANT: OZENERGER, Bradley A.  
 : APPLICANT: HULMES, Jeffrey D.  
 : TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
 : TITLE OF INVENTION: TO OPIOID RECEPTORS  
 : NUMBER OF SEQUENCES: 13  
 :  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: Darby & Darby, P.C.  
 : STREET: 805 Third Avenue  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: USA  
 : ZIP: 10022  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/454,549  
 : FILING DATE: 30-MAY-1995  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Robinson, Joseph R.  
 : REGISTRATION NUMBER: 33,448  
 : REFERENCE/DOCKET NUMBER: 0646/1A818-USS  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 527-7700  
 : TELEFAX: (212) 753-6237  
 : TELEX: 236687  
 :  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2706 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : ORIGINAL SOURCE:  
 : TISSUE TYPE: Rat brain  
 :  
 : US-08-454-549-1

	446	624	506	684	566	744	626	804
QY	CGCTGATATTGTCA	CTTTGTGGTACCC	CTGGTGTCTCCCG	TATGATCATAGAAAT	505			
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QY	ACAATGAGAGACA	CTGTTTAAATTTCA	CAAGAAGCTTGCTT	ACATATGTGAATCA	565			
Db	AAGAGATGAGAGCT	GCTGTGAGATCCT	CGCCCCCTCAGCA	CTATTGGGGCCCTGT	743			
QY	TCACATATATGAT	ATGCAATTTTGTCA	TAGCCGTGCTGTGA	TTCTGTGTTCTTCAGG	625			
Db	CCATGTGATCTTCT	TTTTCCTTCATCAT	CCCTGTGCTGATCAT	CTCTGTCTGACCA	803			
QY	TTTTCATCATTT	636						
Db	GCTTCATGATTT	814						

[illegible]

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1      RESULT 15
2      US-08-454-552-1
3      ; Sequence 1, Application US/08454552
4      ; Patent No. 6005072
5      ; GENERAL INFORMATION:
6      ; APPLICANT: EPPLE, C. Mark
7      ; APPLICANT: OZEMBERGER, Bradley A.
8      ; APPLICANT: HILMES, Jeffrey D.
9      ; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
10     ; TITLE OF INVENTION: TO OPIOID RECEPTORS
11     ; NUMBER OF SEQUENCES: 13
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Darby & Darby, P.C.
14     ; STREET: 805 Third Avenue
15     ; CITY: New York
16     ; STATE: New York
17     ; COUNTRY: USA
18     ; ZIP: 10022
19     ; COMPUTER READABLE FORM:
20     ; MEDIUM TYPE: Floppy disk
21     ; COMPUTER: IBM PC compatible
22     ; OPERATING SYSTEM: PC-DOS/MS-DOS
23     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
24     ; CURRENT APPLICATION DATA:
25     ; APPLICATION NUMBER: US/08/454,552
26     ; FILING DATE: 30-MAY-1995
27     ; CLASSIFICATION: 435
28     ; ATTORNEY/AGENT INFORMATION:
29     ; NAME: Robinson, Joseph R.
30     ; REGISTRATION NUMBER: 33,448
31     ; REFERENCE/DOCKET NUMBER: 0646/1A818-US4
32     ; TELECOMMUNICATION INFORMATION:
33     ; TELEPHONE: (212) 527-7700
34     ; TELEFAX: (212) 753-6237
35     ; TELEX: 236687
36     ; INFORMATION FOR SEQ ID NO: 1:
37     ; SEQUENCE CHARACTERISTICS:
38     ; LENGTH: 2706 base pairs
39     ; TYPE: nucleic acid
40     ;

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; STRANDENESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
;
US-08-454-552-1

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Query Match	6.4%	Score 59.8;	DB 3;	Length 2706;
Best Local Similarity	45.6%	Pred. No. 2.1e-07;		
Matches 251; Conservative	0;	Mismatches 297;	Indels 3;	Gaps 1;

QY	89	GGCTCTACTCTTAAAGGCTTTATTTGGGGGGCTGGTGGG---TGTCAATTCGATCTTTTCC	145
Db	264	GGCTTACTTGGCTGTGTGCATTCGGGGGGCTCTCGGGGAACTGGCTCTGTATATTATGTCA	323
QY	146	TCCTGGTGAATAATGAACACCCGGTCAAGTACCAACCAATGGCGGTCATTAACTTGGTGGTGG	205
Db	324	TCCTCAGGACACCAAGATGTAGAGACAGCTACCAACATTTAACATTTAATCTGGCACTGG	383
QY	206	TCACAGCGTTTTTCTGCTGACAGTGCACATTTTCGCTTGAACCTAATCTCAACAGAACTT	265
Db	384	CTGATATCCCTGGTCTTGTCTAACAATGCCCTTCCAGGGGACAGACATCTCACTGGGCTTCT	443
QY	266	GGATGTTTGGGCGTCCCTTCTGCAATTTGTAGTGGCAATGCTGCACATCCAAATGTACC	325
Db	444	GGCCATTGGGAATGACACTGCACAAACGTCACTTCATTCGACTCACTCAACAAATGTTTA	503
QY	326	TCACGTTCTATTCTATGTGTGATCTGTGCACCAAGATACCTCAATCTTCTTCAAGTCA	385
Db	504	CCAGCACTTTTACTCTGACCCGCCATGAGGTAAACCGCTATGTGGCTATGTGCCACCTTA	563
QY	386	AAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGGCTGCGACTGTGGCATGTGA	445
Db	564	TCCGTGCCCTTGATGTTTGCAGATCTCAGAAAAGCCAGGGCTGTTAATGTGGCCATATGGG	623
QY	446	CGCTGTGATTTGTCAATTGNGTAAACCCCTGTTGTCTCCGGTATGTGAATTCATGAGGAAT	505
Db	624	CCCTGGCTTCAAGTGTGTGGTGTCTCTGTGCCATCAATGGTTATGAGCACAAGTGAAGAATG	683
QY	506	ACAATGAGGAGCACTGTTTAAATTCACAAAAGCTTGCTTACACATATGTGMAAATCA	565
Db	684	AGAGAGTGCAGTGCCTGTGTGAGATCCCTGCCCCCTAGACCTAATTGGGGGCCCTGTATTCG	743
QY	566	TCAACTATATGATAGTCAATTTTGTTCATAGCCGTTGCTGTGATTTCTGTGGTCTTCCAGG	625
Db	744	CCATGTGATCTTCTCTTTTCTCTTCATATCCCTGTGCTGATCACTGTCTGTGCTACA	803
QY	626	TTTTCATCTTT 636	
Db	804	GGCTCATGATTT 814	

Search completed: September 9, 2005, 22:50:16  
Job time : 172.402 secs



Db 1 ATGCAAAATGTGACTTCCCAAGTATGCTGGCCACAAATCTCCAGAAATCTCTTGCC 60  
QY 61 GATCCATATGTGACACCCCACTTAATCAGCTCTACTTCTATGCTTATTTGGCGGGG 120  
Db 61 GATCCATATGTGACACCCCACTTAATCAGCTCTACTTCTATGCTTATTTGGCGGGG 120  
QY 121 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 180  
Db 121 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 180  
QY 181 ATGGCGGTCTATTAATCTGTGGTGTGTCACAGCGTTTCTGTGACAGTGCATTTGCG 240  
Db 181 ATGGCGGTCTATTAATCTGTGGTGTGTCACAGCGTTTCTGTGACAGTGCATTTGCG 240  
QY 241 TTGACCTACTCTCATTAAGTGAAGTGTGATGTTGGGCTGCTTCTGCAAAATTTGAGT 300  
Db 241 TTGACCTACTCTCATTAAGTGAAGTGTGATGTTGGGCTGCTTCTGCAAAATTTGAGT 300  
QY 301 GCCATGCTGCATTCACATGATGATCTCAAGTCTTCTATTTGATGATCTGTGACCC 360  
Db 301 GCCATGCTGCATTCACATGATGATCTCAAGTCTTCTATTTGATGATCTGTGACCC 360  
QY 361 AGATACCTCATCTTCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
Db 361 AGATACCTCATCTTCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
QY 421 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 480  
Db 421 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 480  
QY 481 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGAG 540  
Db 481 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGAG 540  
QY 541 CTGGCTTACATGATGAAATCAATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 541 CTGGCTTACATGATGAAATCAATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 601 GCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 601 GCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 CACTCTTACTATCCACACAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGAG 720  
Db 661 CACTCTTACTATCCACACAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGAG 720  
QY 721 GTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 721 GTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 781 AGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 781 AGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
QY 841 ACAGCAATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
Db 841 ACAGCAATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CAAAAATTAATGCTTATGAAATGTTGTTTGTGCGGT 939  
Db 901 CAAAAATTAATGCTTATGAAATGTTGTTTGTGCGGT 939

## RESULT 2

US-10-085-233B-1  
; Sequence 1, Application US/10085233B  
; Publication No. US2003087249A1  
; GENERAL INFORMATION:  
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA  
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR  
; FILE REFERENCE: MPI2001-021P1RCP1M  
; CURRENT APPLICATION NUMBER: US/10/085,233B

; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/272,677  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1684  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (147)...(1085)  
; OTHER INFORMATION: n at position 1384 can be any  
; OTHER INFORMATION: nucleotide  
US-10-085-233B-1  
Query Match 100.0%; Score 939; DB 14; Length 1684;  
Best Local Similarity 100.0%; Pred. No. 1,4e-270;  
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCAAAATGTGACTTCCCAAGTATGCTGGCCACAAATCTCCAGAAATCTCTTGCC 60  
Db 147 ATGCAAAATGTGACTTCCCAAGTATGCTGGCCACAAATCTCCAGAAATCTCTTGCC 206  
QY 61 GATCCATATGTGACACCCCACTTAATCAGCTCTACTTCTATGCTTATTTGGCGGGG 120  
Db 207 GATCCATATGTGACACCCCACTTAATCAGCTCTACTTCTATGCTTATTTGGCGGGG 266  
QY 121 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 180  
Db 267 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 326  
QY 181 ATGGCGGTCTATTAATCTGTGGTGTGTCACAGCGTTTCTGTGACAGTGCATTTGCG 240  
Db 327 ATGGCGGTCTATTAATCTGTGGTGTGTCACAGCGTTTCTGTGACAGTGCATTTGCG 386  
QY 241 TTGACCTACTCTCATTAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGAT 300  
Db 387 TTGACCTACTCTCATTAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGAT 446  
QY 301 GCCATGCTGCATTCACATGATGATCTCAAGTCTTCTATTTGATGATCTGTGACCC 360  
Db 447 GCCATGCTGCATTCACATGATGATCTCAAGTCTTCTATTTGATGATCTGTGACCC 506  
QY 361 AGATACCTCATCTTCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
Db 507 AGATACCTCATCTTCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 566  
QY 421 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 480  
Db 567 GTGGGTGTCAATTCATTTCTTCTCTCTGTTGAAAATGAAACCCGGTCAAGACACCC 626  
QY 481 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGAG 540  
Db 627 TCCCGGTATGAAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGAG 686  
QY 541 CTGGCTTACATGATGAAATCAATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 687 CTGGCTTACATGATGAAATCAATGATGATGATGATGATGATGATGATGATGATGAT 746  
QY 601 GCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 747 GCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 806  
QY 661 CACTCTTACTATCCACACAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGAG 720  
Db 807 CACTCTTACTATCCACACAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGAG 866  
QY 721 GTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 867 GTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 926  
QY 781 AGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840



Db 927 ACAGATTCATGCTGCTAGACAGAGGTGCAATTTATACGAAATCTTCTAGAGTGA 986  
 Qy 841 ACAGATTCATGCTGCTAGACAGAGGTGCAATTTATAG 900  
 Db 987 ACAGCAATTAATGCTGCTAGATTTCTTCTTTTGGGGAGCCATTTGTTTAA 1046  
 Qy 901 CAAAAGATAATGGCTTATGGAATTTGTTTGGCGT 939  
 Db 1047 CAAAAGATAATGGCTTATGGAATTTGTTTGGCGT 1085

RESULT 3  
 US-10-467-252-52  
 ; Sequence 52. Application US/10467252  
 ; Publication No. US20040115676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
 ; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;  
 ; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;  
 ; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.  
 ; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;  
 ; APPLICANT: HAPALITA, April J.A.; RAMKOMAR, Jayalaxmi;  
 ; APPLICANT: JIN, Pei; TANG, Y. Tom;  
 ; APPLICANT: YUE, Henry; REDDY, Roopa  
 ; APPLICANT: BURFORD, Neil; LU, Dying Aina M.;  
 ; APPLICANT: GRAU, Richard C.; KAHN, Farrah A.;  
 ; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;  
 ; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.  
 ; APPLICANT: WARREN, Bridget A.; YANG, Junming;  
 ; APPLICANT: LEE, Ernestine A.; HARLAND, Lee  
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
 ; FILE REFERENCE: PI-0357 USN  
 ; CURRENT APPLICATION NUMBER: US/10/467,252  
 ; CURRENT FILING DATE: 2003-08-06  
 ; PRIOR APPLICATION NUMBER: PCT/US02/03635  
 ; PRIOR FILING DATE: 2002-02-06  
 ; PRIOR APPLICATION NUMBER: US 60/267,332;  
 ; PRIOR FILING DATE: 2001-02-07  
 ; PRIOR APPLICATION NUMBER: US 60/271,215  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: US 60/274,551  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 60/278,507  
 ; PRIOR FILING DATE: 2001-03-23  
 ; PRIOR APPLICATION NUMBER: US 60/280,597  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/281,107  
 ; PRIOR FILING DATE: 2001-04-02  
 ; PRIOR APPLICATION NUMBER: US 60/282,121  
 ; PRIOR FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 96  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 52  
 ; LENGTH: 1336  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURES:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 90012430CB1  
 ; US-10-467-252-52

Query Match 99.8%; Score 937.4; DB 19; Length 1336;  
 Best Local Similarity 99.9%; Pred. No. 3.7e-270;  
 Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ATGCAAAAATGTGACTTCCCAAGTATGCTGCGCAATACCTCCAGAAATCTCTTGC 60  
 Db 195 ATGCAAAAATGTGACTTCCCAAGTATGCTGCGCAATACCTCCAGAAATCTCTTGC 254  
 Qy 61 GATCTTATAGTGAACCCCACTTAATGAGCTTACTTCAATAGTGTATTATGCGGGCTG 120  
 Db 255 GATCTTATAGTGAACCCCACTTAATGAGCTTACTTCAATAGTGTATTATGCGGGCTG 314

Qy 121 GTGGATGTCATTTTCATTTCTTTCTCTGCTGTAAGAAACACCCGGTCAAGTACACC 180  
 Db 315 GTGGATGTCATTTTCATTTCTTTCTCTGCTGTAAGAAACACCCGGTCAAGTACACC 374  
 Qy 181 ATGGCGGTCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 375 ATGGCGGTCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434  
 Qy 241 TTGACCTACTCTATCAAGAAAGCTTGGATTTTGGGCTGCTTCTGCAATTTTGGAGT 300  
 Db 435 TTGACCTACTCTATCAAGAAAGCTTGGATTTTGGGCTGCTTCTGCAATTTTGGAGT 494  
 Qy 301 GCCATGCTGCAATTCACATGTAACCTGACGTTCTCTATTCATGCTGCAATTCCTGTCACC 360  
 Db 495 GCCATGCTGCAATTCACATGTAACCTGACGTTCTCTATTCATGCTGCAATTCCTGTCACC 554  
 Qy 361 AGATACCTCATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAATCTGATGCT 420  
 Db 555 AGATACCTCATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAATCTGATGCT 614  
 Qy 421 GTGGCTGCGAGTCTGCGATGCGAGCGCTGCTGATTTGTCATTTGCTGACCTCTGTTGTC 480  
 Db 615 GTGGCTGCGAGTCTGCGATGCGAGCGCTGCTGATTTGTCATTTGCTGACCTCTGTTGTC 674  
 Qy 481 TCCCGGTAATGGAATTCATGAGAAATCAATGAGAGACGCTTTAAATTTCAAAAGAG 540  
 Db 675 TCCCGGTAATGGAATTCATGAGAAATCAATGAGAGACGCTTTAAATTTCAAAAGAG 734  
 Qy 541 CTGCTTACATATGATGGAATTCATCAATCAATATATATAGTCAATTTTGTCAATAGCGCTT 600  
 Db 735 CTGCTTACATATGATGGAATTCATCAATCAATATATATAGTCAATTTTGTCAATAGCGCTT 794  
 Qy 601 GCTGTGATTTCTGTTGCTTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAGCTACGC 660  
 Db 795 GCTGTGATTTCTGTTGCTTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAGCTACGC 854  
 Qy 661 CACTCTTTCTATCCCAACAGAGGCTCTGGGCTCACTGAGAAACCTATTTTATATAGG 720  
 Db 855 CACTCTTTCTATCCCAACAGAGGCTCTGGGCTCACTGAGAAACCTATTTTATATAGG 914  
 Qy 721 GTCATCTTGTGTTGTTCTTCCCTACAGTCTTATAGTATATATATATATATATATATAT 780  
 Db 915 GTCATCTTGTGTTGTTCTTCCCTACAGTCTTATAGTATATATATATATATATATATAT 974  
 Qy 781 ACAGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 Db 975 ACAGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034  
 Qy 841 ACAGCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 Db 1035 ACAGCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094  
 Qy 901 CAAAAGATAATGGCTTATGGAATTTGTTTGGCGT 939  
 Db 1095 CAAAAGATAATGGCTTATGGAATTTGTTTGGCGT 1133

RESULT 4  
 US-10-467-252-53  
 ; Sequence 53. Application US/10467252  
 ; Publication No. US20040115676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
 ; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;  
 ; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;  
 ; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.  
 ; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;  
 ; APPLICANT: HAPALITA, April J.A.; RAMKOMAR, Jayalaxmi;  
 ; APPLICANT: JIN, Pei; TANG, Y. Tom;  
 ; APPLICANT: YUE, Henry; REDDY, Roopa  
 ; APPLICANT: BURFORD, Neil; LU, Dying Aina M.;  
 ; APPLICANT: GRAU, Richard C.; KAHN, Farrah A.;

```

; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junning;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incycle ID No: 90012586CB1
US-10-467-252-53
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Query Match      98.8%; Score 928.2; DB 19; Length 1340;
Best Local Similarity 99.7%; Pred. No. 2.2e-267;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAANGAGCTTCCCAAGTATGCGGCGCACATACCTCCAGGAATTCCTTGCGATCCCT 66
Db 205 ACGAGTACTTCCCAAGTATGCGGCGCACATACCTCCAGGAATTCCTTGCGATCCCT 264
QY 67 ATAGTACACCCCACTTAATCAAGCTCTTACTTCAATAGTGTCTTATTTGGCGGGCTGTGGGT 126
Db 265 ATAGTACACCCCACTTAATCAAGCTCTTACTTCAATAGTGTCTTATTTGGCGGGCTGTGGGT 324
QY 127 GTCAATTCATTTCTTTCTCTCTGCGTGAATAATGAACACCGGTCAGTGAACCACTATGGCG 186
Db 325 GTCAATTCATTTCTTTCTCTCTGCGTGAATAATGAACACCGGTCAGTGAACCACTATGGCG 384
QY 187 GTCAATTAAGTTGGTGGTGTCCACAGGCTTTTCTGTGACAGTGCATTTGCTTGACC 246
Db 385 GTCAATTAAGTTGGTGGTGTCCACAGGCTTTTCTGTGACAGTGCATTTGCTTGACC 444
QY 247 TACCTCATCAAGAAGACTTGTGATGTTGGCTGCGCTTCTGCAAAATTTGTAGTGCATG 306
Db 445 TACCTCATCAAGAAGACTTGTGATGTTGGCTGCGCTTCTGCAAAATTTGTAGTGCATG 504
QY 307 CTGACATCCACATGTAAGTCTCAAGTCTTCTATTTCTATGTGTGATCTGTGACCAAGATAC 366
Db 505 CTGACATCCACATGTAAGTCTCAAGTCTTCTATTTCTATGTGTGATCTGTGACCAAGATAC 564
QY 367 CTGATCTCTTCAAGGCAAGAACAAGTGAATTTCAAGAAATTCGATGCGTGTGGCT 426
Db 565 CTGATCTCTTCAAGGCAAGAACAAGTGAATTTCAAGAAATTCGATGCGTGTGGCT 624
QY 427 GCCAGTCTGGCAATGTGAAGCTGTGATTTGTCAATTTGTGATCCCTGTGTCTCCCGG 486
Db 625 GCCAGTCTGGCAATGTGAAGCTGTGATTTGTCAATTTGTGATCCCTGTGTCTCCCGG 684
QY 487 TATGGAATCCATGAGGAATACATGAGAGACCTGTTTAATTTCAAAAAGCTTTGCT 546
Db 1105 TATGGAATCCATGAGGAATACATGAGAGACCTGTTTAATTTCAAAAAGCTTTGCT 546
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Db 685 TATGGAATCCATGAGGAATACATGAGAGACCTGTTTAATTTCAAAAAGCTTTGCT 744
QY 547 TACACATATGTGAAATCATCAACTATATGATGATCATTTTGTGCATAGCCGTTGCTGTG 606
Db 745 TACACATATGTGAAATCATCAACTATATGATGATCATTTTGTGCATAGCCGTTGCTGTG 804
QY 607 ATTCTGTGTGCTTCCAGGCTTTCATCATATATGTGATGTGTCAGAAAGTCAAGCCACTCT 666
Db 805 ATTCTGTGTGCTTCCAGGCTTTCATCATATATGTGATGTGTCAGAAAGTCAAGCCACTCT 864
QY 667 TTAATATCCACAGAGAGTTCTGGGCTGACGTCGAAAGAAACCTATTTTAAAGGGGTCAAC 726
Db 865 TTAATATCCACAGAGAGTTCTGGGCTGACGTCGAAAGAAACCTATTTTAAAGGGGTCAAC 924
QY 727 CTGTGTTGTTCTCTTCCCTACAGTCTTTAGATCTATTAATCTTGATGTGTGACGAT 786
Db 925 CTGTGTTGTTCTCTTCCCTACAGTCTTTAGATCTATTAATCTTGATGTGTGACGAT 984
QY 787 TCCATATGCTGTAGACAGAAAGTTGATTTTAAAGAAATCTTCTTGAGTGAACAGCA 846
Db 985 TCCATATGCTGTAGACAGAAAGTTGATTTTAAAGAAATCTTCTTGAGTGAACAGCA 1044
QY 847 ATTAGCTGTATGATGATTTGCTTCTTGTCTTTGGGGAAGCAATGTTTAAGCAAAAG 906
Db 1045 ATTAGCTGTATGATGATTTGCTTCTTGTCTTTGGGGAAGCAATGTTTAAGCAAAAG 1104
QY 907 ATTAATGGCTTATGGAATGTGTTTGTGCGCT 939
Db 1105 ATTAATGGCTTATGGAATGTGTTTGTGCGCT 1137

RESULT 5
US-10-467-252-54
; Sequence 54, Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAMLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HARALDA, April J.A.; RAMKOMAR, Jayalakshmi;
; APPLICANT: JIN, Pei; YANG, Y.Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dying, Aina M.;
; APPLICANT: GRAU, Richard C.; KAHN, Parrah A.;
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junning;
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 54
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LENGTH: 1460  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 90012670CB1  
US-10-467-252-54

Query Match 98.8%; Score 928.2; DB 19; Length 1460;  
Best Local Similarity 99.7%; Pred. No. 2.3e-267;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 AAATGACATCTCCCAAGATGCTGGGCAACATCTCCAGGAATCTCTTGGAATCCT 66  
325 ACAGGTATCTCCCAAGATGCTGGGCAACATCTCCAGGAATCTCTTGGAATCCT 384  
67 ATATGACACCCCACTTAATCAGCTCTACTTCAATGCTTATTTGGCGGGTGGT 126  
385 ATATGACACCCCACTTAATCAGCTCTACTTCAATGCTTATTTGGCGGGTGGT 444  
127 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 186  
445 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 504  
187 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 246  
505 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 564  
247 TACCTCATCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTGCCATG 306  
565 TACCTCATCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTGCCATG 624  
307 CTGCAATTCATCAATGATCTCACTTCTTATTTGATGCTGATCTGTCACCAAT 366  
625 CTGCAATTCATCAATGATCTCACTTCTTATTTGATGCTGATCTGTCACCAAT 684  
367 CTCAATCTCTCAAGTCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTG 426  
685 CTCAATCTCTCAAGTCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTG 744  
427 GCCAGTCTGCAATGATGAGCGCTGATGTTGCTATTTGAGTACCCCTGTTGCTCC 486  
745 GCCAGTCTGCAATGATGAGCGCTGATGTTGCTATTTGAGTACCCCTGTTGCTCC 804  
487 TATGGAATCCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAAAGACTTGT 546  
805 TATGGAATCCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAAAGACTTGT 864  
547 TACCATATGGAATAATCACTATATATGATGCTATTTTGTCAATGAGCGTGTG 606  
865 TACCATATGGAATAATCACTATATATGATGCTATTTTGTCAATGAGCGTGTG 924  
607 ATTCTGTTGCTCTCCAGTCTTCAATATGTTGATGAGTGAAGTACAGCACTCT 666  
925 ATTCTGTTGCTCTCCAGTCTTCAATATGTTGATGAGTGAAGTACAGCACTCT 984  
667 TTAATATCCACCAAGAGTCTGAGCTCACTGTAATAAATCTTATTTTAAAGAGTATC 726  
985 TTAATATCCACCAAGAGTCTGAGCTCACTGTAATAAATCTTATTTTAAAGAGTATC 1044  
727 CTGTTGTTGCTCTCCAGTCTTCAATATGTTGATGCTATTTTGTCAATGAGCGTGT 786  
1045 CTGTTGTTGCTCTCCAGTCTTCAATATGTTGATGCTATTTTGTCAATGAGCGTGT 1104  
787 TCCAAATGCTGAGCAAGAGTGTGATTTTAAATCAATCTCTGATGATGATGATG 846  
1105 TCCAAATGCTGAGCAAGAGTGTGATTTTAAATCAATCTCTGATGATGATGATG 1164  
847 ATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906  
1165 ATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1224  
907 ATTAATGCTTATGGAATGTTGTTTGTGCGCT 939

Db 1225 ATTAATGCTTATGGAATGTTGTTTGTGCGCT 1257

RESULT 6  
US-09-782-974C-81  
Sequence 81, Application US/09782974C  
Publication No. US20030082534A1  
GENERAL INFORMATION:  
APPLICANT: Vogeli, Gabriel  
APPLICANT: Lind, Peter  
APPLICANT: Wood, Linda S.  
APPLICANT: Parodi, Luis A.  
TITLE OR INVENTION: No. US20030082534A1 G Protein Coupled Receptor  
FILE REFERENCE: 41USPHRM311  
CURRENT APPLICATION NUMBER: US/09/782,974C  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 60/165,838  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 09/714,449  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 60/198,568  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: 60/166,071  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/166,678  
PRIOR FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: 60/173,396  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/184,129  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: 60/185,421  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/185,554  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/186,530  
PRIOR FILING DATE: 2000-03-02  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 81  
LENGTH: 2525  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-782-974C-81

Query Match 98.8%; Score 928.2; DB 10; Length 2525;  
Best Local Similarity 99.7%; Pred. No. 3.2e-267;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 AAATGACATCTCCCAAGATGCTGGGCAACATCTCCAGGAATCTCTTGGAATCCT 66  
9 ACAGGTATCTCCCAAGATGCTGGGCAACATCTCCAGGAATCTCTTGGAATCCT 68  
67 ATATGACACCCCACTTAATCAGCTCTACTTCAATGCTTATTTGGCGGGTGGT 126  
69 ATATGACACCCCACTTAATCAGCTCTACTTCAATGCTTATTTGGCGGGTGGT 128  
127 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 186  
129 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 188  
187 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 246  
189 GTCAATTCATCTTTCTCTCTGTAATAAAGACCCGGTCAATGACCAATGGCG 248  
247 TACCTCATCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTGCCATG 306  
249 TACCTCATCAAGAAAGCTTGATGTTGGCTGCTCTGCAATTTGAGTGCCATG 308  
307 CTGCAATTCATCAATGATCTCACTTCTTATTTGATGCTGATCTGTCACCAAT 366  
309 CTGCAATTCATCAATGATCTCACTTCTTATTTGATGCTGATCTGTCACCAAT 368

QY 367 CTCATCTTCTTCAAGTGCAAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGTGGCT 426  
| | | | |  
Db 369 CTCATCTTCTTCAAGTGCAAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGTGGCT 428  
| | | | |  
QY 427 GCCAGTCTGGCATGTGAGACGCTGTGATTCATTGTGGTACCCCTGTGTCTCCCG 486  
| | | | |  
Db 429 GCCAGTCTGGCATGTGAGACGCTGTGATTCATTGTGGTACCCCTGTGTCTCCCG 488  
| | | | |  
QY 487 TATGGAATCCATAGGAATTCATAGAGAGACCTGTTTAAATTTACAAAAGCTTGTCT 546  
| | | | |  
Db 489 TATGGAATCCATAGGAATTCATAGAGAGACCTGTTTAAATTTACAAAAGCTTGTCT 548  
| | | | |  
QY 547 TACACATATGTGAAAATTCATCACTATATGATGATCTTTTGTCAAGCCGTGTGTG 606  
| | | | |  
Db 549 TACACATATGTGAAAATTCATCACTATATGATGATCTTTTGTCAAGCCGTGTGTG 608  
| | | | |  
QY 607 ATTCTGTGTGCTTCCAGGTCCTTCATCATTATGTGATGTGAGAAAGCTACGCCACTCT 666  
| | | | |  
Db 609 ATTCTGTGTGCTTCCAGGTCCTTCATCATTATGTGATGTGAGAAAGCTACGCCACTCT 668  
| | | | |  
QY 667 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCTATC 726  
| | | | |  
Db 669 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCTATC 728  
| | | | |  
QY 727 CTGTGTGTGCTTCCCTTCCACAGTCTTTAGAGATCTATTAATGATGTGTGAGAGCAT 786  
| | | | |  
Db 729 CTGTGTGTGCTTCCCTTCCACAGTCTTTAGAGATCTATTAATGATGTGTGAGAGCAT 788  
| | | | |  
QY 787 TCCAAATGCTGTGACGCAAGTGTGATTTATACGAAATCTTCTTGAAGTGTACAGCA 846  
| | | | |  
Db 789 TCCAAATGCTGTGACGCAAGTGTGATTTATACGAAATCTTCTTGAAGTGTACAGCA 848  
| | | | |  
QY 847 ATTAGCGTGATGATTTGCTCTCTTGTCTTGGGGGAAAGCATGTGTTTAAAGCAAAAG 906  
| | | | |  
Db 849 ATTAGCGTGATGATTTGCTCTCTTGTCTTGGGGGAAAGCATGTGTTTAAAGCAAAAG 908  
| | | | |  
QY 907 ATTAATGGCTTATGAAATGTGTGTTGTGGCCGT 939  
| | | | |  
Db 909 ATTAATGGCTTATGAAATGTGTGTTGTGGCCGT 941  
| | | | |  
RESULT 7  
US-10-467-492A-81  
; Sequence 81, Application US/10467492A  
; Publication No. US200506976A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn Company  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein Coupled Receptor  
; FILE REFERENCE: 0411PHEM313  
; CURRENT APPLICATION NUMBER: US/10/467,492A  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 81  
; LENGTH: 2525  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-467-492A-81

Query Match 98.8%; Score 928.2; DB 21; Length 2525;  
Best Local Similarity 99.7%; Pred. No. 3.2e-267;  
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAATGTGACTTCCCAAGTATGCTGGGCAACAATACCTCCAGAAATCTCTTGCAATCCT 66  
| | | | |  
Db 9 ACGAGTGACTTCCCAAGTATGCTGGGCAACAATACCTCCAGAAATCTCTTGCAATCCT 68  
| | | | |  
QY 67 ATAGTGACACCCCACTTAATCAAGCTCTACTCATAGTGTCTTATGCGGGCTGTGGGT 126  
| | | | |

Db 69 ATAGTGACACCCCACTTAATCAAGCTCTACTCATAGTGTCTTATGCGGGCTGTGGGT 128  
| | | | |  
QY 127 GTCAATTCATCTTTTCTCTCTGTGGAATAAGAACACCCGGTCACTGACACCAATGGG 186  
| | | | |  
Db 129 GTCAATTCATCTTTTCTCTCTGTGGAATAAGAACACCCGGTCACTGACACCAATGGG 188  
| | | | |  
QY 187 GTCAATTCATCTTTTCTCTCTGTGGAATAAGAACACCCGGTCACTGACACCAATGGG 246  
| | | | |  
Db 189 GTCAATTCATCTTTTCTCTCTGTGGAATAAGAACACCCGGTCACTGACACCAATGGG 248  
| | | | |  
QY 247 TACCTCATCAAGAAAGCTTGAATGTTTGGGCTGCCCTTCGCAAAATTTGTAGTGCATG 306  
| | | | |  
Db 249 TACCTCATCAAGAAAGCTTGAATGTTTGGGCTGCCCTTCGCAAAATTTGTAGTGCATG 308  
| | | | |  
QY 307 CTGCAATCCACATGATGACTCAGCTTCCATCTATGTATGTGTATCTGTGTACCAAGATAC 366  
| | | | |  
Db 309 CTGCAATCCACATGATGACTCAGCTTCCATCTATGTATGTGTATCTGTGTACCAAGATAC 368  
| | | | |  
QY 367 CTCATCTTCTTCAAGTGCAAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGTGGCT 426  
| | | | |  
Db 369 CTCATCTTCTTCAAGTGCAAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGTGGCT 428  
| | | | |  
QY 427 GCCAGTCTGGCATGTGAGACGCTGTGATTCATTGTGGTACCCCTGTGTCTCCCG 486  
| | | | |  
Db 429 GCCAGTCTGGCATGTGAGACGCTGTGATTCATTGTGGTACCCCTGTGTCTCCCG 488  
| | | | |  
QY 487 TATGGAATCCATAGGAATTCATAGAGAGACCTGTTTAAATTTACAAAAGCTTGTCT 546  
| | | | |  
Db 489 TATGGAATCCATAGGAATTCATAGAGAGACCTGTTTAAATTTACAAAAGCTTGTCT 548  
| | | | |  
QY 547 TACACATATGTGAAAATTCATCACTATATGATGATCTTTTGTCAAGCCGTGTGTG 606  
| | | | |  
Db 549 TACACATATGTGAAAATTCATCACTATATGATGATCTTTTGTCAAGCCGTGTGTG 608  
| | | | |  
QY 607 ATTCTGTGTGCTTCCAGGTCCTTCATCATTATGTGATGTGAGAAAGCTACGCCACTCT 666  
| | | | |  
Db 609 ATTCTGTGTGCTTCCAGGTCCTTCATCATTATGTGATGTGAGAAAGCTACGCCACTCT 668  
| | | | |  
QY 667 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCTATC 726  
| | | | |  
Db 669 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCTATC 728  
| | | | |  
QY 727 CTGTGTGTGCTTCCCTTCCACAGTCTTTAGAGATCTATTAATGATGTGTGAGAGCAT 786  
| | | | |  
Db 729 CTGTGTGTGCTTCCCTTCCACAGTCTTTAGAGATCTATTAATGATGTGTGAGAGCAT 788  
| | | | |  
QY 787 TCCAAATGCTGTGACGCAAGTGTGATTTATACGAAATCTTCTTGAAGTGTACAGCA 846  
| | | | |  
Db 789 TCCAAATGCTGTGACGCAAGTGTGATTTATACGAAATCTTCTTGAAGTGTACAGCA 848  
| | | | |  
QY 847 ATTAGCGTGATGATTTGCTCTCTTGTCTTGGGGGAAAGCATGTGTTTAAAGCAAAAG 906  
| | | | |  
Db 849 ATTAGCGTGATGATTTGCTCTCTTGTCTTGGGGGAAAGCATGTGTTTAAAGCAAAAG 908  
| | | | |  
QY 907 ATTAATGGCTTATGAAATGTGTGTTGTGGCCGT 939  
| | | | |  
Db 909 ATTAATGGCTTATGAAATGTGTGTTGTGGCCGT 941  
| | | | |

RESULT 8  
US-10-975-979-81  
; Sequence 81, Application US/10975979  
; Publication No. US20050112660A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Huff, Rita  
; APPLICANT: Sejlitz, Torsten  
; APPLICANT: Lind, Peter  
; APPLICANT: Slightom, Jerry  
; APPLICANT: Scheinin, Kathleen  
; APPLICANT: Ruff, Valerie

```

; APPLICANT: Kaytee, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Parodi, Luis
; APPLICANT: Hiebsch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PHRM293
; CURRENT APPLICATION NUMBER: US/10/975,979
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-975-979-81

Query Match      98.8%; Score 928.2; DB 21; Length 2525;
Best Local Similarity 99.7%; Pred. No. 3.2e-267;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTTGCGATCT 66
DB 9 ACAGGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTTGCGATCT 68
QY 67 ATAGTGAACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTT 126
DB 69 ATAGTGAACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTT 128
QY 127 GTGATTTCCATTTTTCCTCCCTGCGTGAATAATGAACACCCGGTCACTGACCACTAGCG 186
DB 129 GTGATTTCCATTTTTCCTCCCTGCGTGAATAATGAACACCCGGTCACTGACCACTAGCG 188
QY 187 GTGATTTCCATTTTTCCTCCCTGCGTGAATAATGAACACCCGGTCACTGACCACTAGCG 246
DB 189 GTGATTTCCATTTTTCCTCCCTGCGTGAATAATGAACACCCGGTCACTGACCACTAGCG 248
QY 247 TACCTCATCAAGAAAGCTTGATGTTGGGCTGCCCTTTCGCAAAATTTGTAGTGCATG 306
DB 249 TACCTCATCAAGAAAGCTTGATGTTGGGCTGCCCTTTCGCAAAATTTGTAGTGCATG 308
QY 307 CTGCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
DB 309 CTGCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
QY 367 CTGATCTTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGCT 426
DB 369 CTGATCTTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGCT 428
QY 427 GCCAGTGTGGCATGTGAGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 486
DB 429 GCCAGTGTGGCATGTGAGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 488
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QY 487 TATGAAATCCATGAGAAATCAATGAGAGACTGTTTAAATTTCAAAAGACTTGTCT 546
DB 489 TATGAAATCCATGAGAAATCAATGAGAGACTGTTTAAATTTCAAAAGACTTGTCT 548
QY 547 TACAAATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGATGAT 606
DB 549 TACAAATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGATGAT 608
QY 607 ATTCTGTGGTCTTCCAGGCTTCACTATGATGATGATGATGATGATGATGATGATGATGAT 666
DB 609 ATTCTGTGGTCTTCCAGGCTTCACTATGATGATGATGATGATGATGATGATGATGATGAT 668
QY 667 TTACTATCCCAACGAGAGTCTGGGCTCAGCTGAAACCTATTTTATATGAGGCTCATC 726
DB 669 TTACTATCCCAACGAGAGTCTGGGCTCAGCTGAAACCTATTTTATATGAGGCTCATC 728
QY 727 CTGTTGTTGTTCCCTCCCTCAACAGTCTTTAGGATCTATTAATGATGATGATGATGATGAT 786
DB 729 CTGTTGTTGTTCCCTCCCTCAACAGTCTTTAGGATCTATTAATGATGATGATGATGATGAT 788
QY 787 TCCAAATGCTGTGAGCAAGAGTTCATTTTATTAAGAAATCTTCTTGAAGTGAACGCA 846
DB 789 TCCAAATGCTGTGAGCAAGAGTTCATTTTATTAAGAAATCTTCTTGAAGTGAACGCA 848
QY 847 ATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
DB 849 ATTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 908
QY 907 ATATGCTTATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
DB 909 ATATGCTTATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 941
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RESULT 9
US-10-017-161-1193
; Sequence 1193, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1318)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1118)
; US-10-017-161-1193
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Query Match      98.8%; Score 927.8; DB 15; Length 1318;
Best Local Similarity 99.8%; Pred. No. 2.8e-267;
Matches 929; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTTGCGATCTCTAT 68
DB 185 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCTTGCGATCTCTAT 244
QY 69 ATGTAACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 128
DB 245 ATGTAACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 304
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QY 609 TCTGTGCTCTCCAGAGTCTTCATCATATGATGTGAGGAGGAGTACGCCACTCTTT 668  
DB 12124 TCTGTGCTCTCCAGAGTCTTCATCATATGATGTGAGGAGGAGTACGCCACTCTTT 12183  
QY 669 ACTATCCACAGAGAGTCTGAGGCTGAGCTGAGAAAACTATTTTATAGGGGTCATCT 728  
DB 12184 ACTATCCACAGAGAGTCTGAGGCTGAGCTGAGAAAACTATTTTATAGGGGTCATCT 12243  
QY 729 TGTGTGCTCTCCAGAGTCTTCATCATATGATGTGAGGAGGAGTACGCCACTCT 788  
DB 12244 TGTGTGCTCTCCAGAGTCTTCATCATATGATGTGAGGAGGAGTACGCCACTCT 12303  
QY 789 CAATGCTGTAGAGAGAGTGTGATTTATAGAAATCTCTTGAAGTGTAGAGCAAT 848  
DB 12304 CAATGCTGTAGAGAGAGTGTGATTTATAGAAATCTCTTGAAGTGTAGAGCAAT 12363  
QY 849 TAGCTGTATGATTTGCTCTCTTTGTTGGGGAGAGCCATGTTTAAAGCAAAAGAT 908  
DB 12364 TAGCTGTATGATTTGCTCTCTTTGTTGGGGAGAGCCATGTTTAAAGCAAAAGAT 12423  
QY 909 AATTGGCTTATGAAATGTCTTTGTGCGCT 939  
DB 12424 AATTGGCTTATGAAATGTCTTTGTGCGCT 12454

RESULT 11  
US-09-995-225-3  
; Sequence 3, Application US/09995225  
; Publication No. US20020193584A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Hong T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Pride, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
; FILE REFERENCE: AREN-0308  
; CURRENT APPLICATION NUMBER: US/09/995, 225  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170, 496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253, 404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255, 366  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/270, 286  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282, 365  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/270, 266  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282, 032  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282, 358  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282, 356  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/290, 917  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/309, 208  
; PRIOR FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-995-225-3

Query Match 97.3%; Score 913.4; DB 9; Length 918;

Best Local Similarity 99.9%; Pred. No. 4,8e-263;  
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATGCTGGCCCAATATCTCCAGAAATCTCTTGCATCTTAATAGTACACCCACTTA 84  
DB 1 ATGCTGGCCCAATATCTCCAGAAATCTCTTGCATCTTAATAGTACACCCACTTA 60  
QY 85 ATGAGCTCTTACTTATATAGTCTTATTTGGGGGCTGGTGGGTGATTTTCAATCTTTTC 144  
DB 61 ATGAGCTCTTACTTATATAGTCTTATTTGGGGGCTGGTGGGTGATTTTCAATCTTTTC 120  
QY 145 CTCTGTGAAAATGAAACACCCGGTGTAGAACACATGCGGGCTTAACTTAACTTGGTGTG 204  
DB 121 CTCTGTGAAAATGAAACACCCGGTGTAGAACACATGCGGGCTTAACTTAACTTGGTGTG 180  
QY 205 GTCCACAGCGTCTTCTGTGACAGTGCATTTTCTGTGACCTTACCTTCAATCAAGAACT 264  
DB 181 GTCCACAGCGTCTTCTGTGACAGTGCATTTTCTGTGACCTTACCTTCAATCAAGAACT 240  
QY 265 TGGATGTTTGGGCTGCCCTTCTGCAATTTTGTAGTCCATGCTGCATCCACATGTAC 324  
DB 241 TGGATGTTTGGGCTGCCCTTCTGCAATTTTGTAGTCCATGCTGCATCCACATGTAC 300  
QY 325 CTCAGTTCCTATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 384  
DB 301 CTCAGTTCCTATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
QY 385 AAAGACAAAGTGAATTTCTACAGAAATCTGACAGTGTGCTGACAGTGTGCTGACAGT 444  
DB 361 AAAGACAAAGTGAATTTCTACAGAAATCTGACAGTGTGCTGACAGTGTGCTGACAGT 420  
QY 445 ACGTGTGATTTGTCTATTTGTGTAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 504  
DB 421 ACGTGTGATTTGTCTATTTGTGTAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 505 TACATGAGAGAGACGTTTAAATTTCAAAAGAGCTTCTACATATGAGAAATC 564  
DB 481 TACATGAGAGAGACGTTTAAATTTCAAAAGAGCTTCTACATATGAGAAATC 540  
QY 565 ATCAACTATATGATGATGATTTTGTATAGCGTGTGCTGATGCTGATGCTGCTG 624  
DB 541 ATCAACTATATGATGATGATTTTGTATAGCGTGTGCTGATGCTGATGCTGATGCTG 600  
QY 625 GTCTTATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
DB 601 GTCTTATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
QY 685 TTCTGGGCTCAGCTGAAAACTATTTTATAGGGGTATCTTGTGTTTCTTCC 744  
DB 661 TTCTGGGCTCAGCTGAAAACTATTTTATAGGGGTATCTTGTGTTTCTTCC 720  
QY 745 TACAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 804  
DB 721 TACAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
QY 805 AAGGTGATTTTATATAGAAATCTTCTGATGATGATGATGATGATGATGATGATG 864  
DB 781 AAGGTGATTTTATATAGAAATCTTCTGATGATGATGATGATGATGATGATGATG 840  
QY 865 CTCTCTCTTGTCTTTGGGGAGAGCCATGTTTAAAGCAAAAGTATTTGGCTTATGAA 924  
DB 841 CTCTCTCTTGTCTTTGGGGAGAGCCATGTTTAAAGCAAAAGTATTTGGCTTATGAA 900  
QY 925 TGTGTTTGTGCGCT 939  
DB 901 TGTGTTTGTGCGCT 915

RESULT 12  
US-09-995-225-3  
; Sequence 3, Application US/09995225  
; Publication No. US20030193584A9  
; GENERAL INFORMATION:



```

1  APPLICANT: Chen, Ruoping
2  APPLICANT: Chu, Zhi Liang
3  APPLICANT: Dang, Huong T.
4  APPLICANT: Lowitz, Kevin P.
5  APPLICANT: Priddy, Cameron
6  TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
7  TITLE OF INVENTION: Receptors
8  FILE REFERENCE: AREN-0308
9  CURRENT APPLICATION NUMBER: US/09/995,225
10 CURRENT FILING DATE: 2001-11-26
11 PRIOR APPLICATION NUMBER: 09/170,496
12 PRIOR FILING DATE: 1998-10-13
13 PRIOR APPLICATION NUMBER: PCT/US99/23938
14 PRIOR FILING DATE: 1998-10-13
15 PRIOR APPLICATION NUMBER: 60/253,404
16 PRIOR FILING DATE: 2000-11-27
17 PRIOR APPLICATION NUMBER: 60/255,366
18 PRIOR FILING DATE: 2000-12-12
19 PRIOR APPLICATION NUMBER: 60/270,286
20 PRIOR FILING DATE: 2001-02-20
21 PRIOR APPLICATION NUMBER: 60/282,365
22 PRIOR FILING DATE: 2001-04-06
23 PRIOR APPLICATION NUMBER: 60/270,266
24 PRIOR FILING DATE: 2001-02-20
25 PRIOR APPLICATION NUMBER: 60/282,032
26 PRIOR FILING DATE: 2001-04-06
27 PRIOR APPLICATION NUMBER: 60/282,358
28 PRIOR FILING DATE: 2001-04-06
29 PRIOR APPLICATION NUMBER: 60/282,356
30 PRIOR FILING DATE: 2001-04-06
31 PRIOR APPLICATION NUMBER: 60/290,917
32 PRIOR FILING DATE: 2001-05-14
33 PRIOR APPLICATION NUMBER: 60/309,208
34 PRIOR FILING DATE: 2001-07-31
35 NUMBER OF SEQ ID NOS: 67
36 SOFTWARE: PatentIn version 3.1
37 SEQ ID NO 3
38 LENGTH: 918
39 TYPE: DNA
40 ORGANISM: Homo sapiens
41 US-09-995-225-3
42
43 Query Match 97.3%; Score 913.4; DB 10; Length 918;
44 Best Local Similarity 99.9%; Pred. No. 4.8e-263;
45 Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
46
47 25 ATGCGTCGCCCACTACCTCCAGGAATTCCTCTTGCAATCTCTATAGAGACACCCACTTA 84
48 1 ATGCGTCGCCCACTACCTCCAGGAATTCCTCTTGCAATCTCTATAGAGACACCCACTTA 60
49
50 85 ATCAGCCCTCTATCTATAGTGTCTTATTTGGCGGGCTGTGGTGTCTATTTCCATTCTTTTC 144
51 ATCAGCCCTCTATCTATAGTGTCTTATTTGGCGGGCTGTGGTGTCTATTTCCATTCTTTTC 120
52
53 145 CTCCTGTGAAATAAGAACACCCGGTCACTGACACCAATGCGGTCATTAACTTGTGTGTG 204
54 CTCCTGTGAAATAAGAACACCCGGTCACTGACACCAATGCGGTCATTAACTTGTGTGTG 180
55
56 205 GTCACAGACGGTTTTTCTGCTGACAGTGCATTTTGGCTTGAACCTTACATGAAAGAACT 264
57 GTCACAGACGGTTTTTCTGCTGACAGTGCATTTTGGCTTGAACCTTACATGAAAGAACT 240
58
59 265 TGGATGTTTGGGGCTGCGCCCTTCGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 324
60 TGGATGTTTGGGGCTGCGCCCTTCGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
61
62 325 CTCACGTTCTATTCTATGTGTGATCCTGCTGACCAAGATACCTATCTTTCAGATGC 384
63 CTCACGTTCTATTCTATGTGTGATCCTGCTGACCAAGATACCTATCTTTCAGATGC 360
64
65 385 AAAGCAAAAGTGAATTCTTACAGAAAACGTGATGCTGTGGCTGCAGTGTGCGATGTGG 444
66 AAAGCAAAAGTGAATTCTTACAGAAAACGTGATGCTGTGGCTGCAGTGTGCGATGTGG 420
67
68 361 AAAGCAAAAGTGAATTCTTACAGAAAACGTGATGCTGTGGCTGCAGTGTGCGATGTGG 420

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QY	445	ACGCTGCTGATTTGCATTTGGTGTACCCCTGGTTGTCTCCCGGTATGCAATCCATGAGGAA	504
Db	421	ACGCTGGATGATTTGCATTTGGTGTACCCCTGGTTGTCTCCCGGTATGCAATCCATGAGGAA	480
QY	505	TACATATGAGGAGCACTGTTTTAAATTTTCACAAAAGAGCTTGCTTACATATGTGMAATC	564
Db	481	TACATATGAGGAGCACTGTTTTAAATTTTCACAAAAGAGCTTGCTTACATATGTGMAATC	540
QY	565	ATCAACTATATGATAGTCAATTTTTTGTCAAGACCGGTGTGTGATTTGTTGGTCTTCAG	624
Db	541	ATCAACTATATGATAGTCAATTTTTTGTCAAGACCGGTGTGTGATTTGTTGGTCTTCAG	600
QY	625	GTTCTTCATCATATATGTTGATATGTGTGACAGAGTACAGCCACTTTTACATATCCACACAGAG	684
Db	601	GTTCTTCATCATATATGTTGATATGTGTGACAGAGTACAGCCACTTTTACATATCCACACAGAG	660
QY	685	TTCTGGGCTCAGCTGAAAAACCTATATTTTTTTTATAGGAGGTCATCTTGTTTGTTCCTTCCC	744
Db	661	TTCTGGGCTCAGCTGAAAAACCTATATTTTTTTTATAGGAGGTCATCTTGTTTGTTCCTTCCC	720
QY	745	TACCAAGTCTTTAGAGATCTATTTACTTGAATGTGTGACGCAATTCOAATGCTGTAGCAGC	804
Db	721	TACCAAGTCTTTAGAGATCTATTTACTTGAATGTGTGACGCAATTCOAATGCTGTAGCAGC	780
QY	805	AAGGTGATTTTATTAACGAATCTCTCTGAGTGTATACAGAAATTAAGCTGTATGATTTG	864
Db	781	AAGGTGATTTTATTAACGAATCTCTCTGAGTGTATACAGAAATTAAGCTGTATGATTTG	840
QY	865	CTTCTCTTTTGTCTTTGGGGGAGAGCCATTGGTTTAAGCAAAAGATTAATGGCTTATGGAAT	924
Db	841	CTTCTCTTTTGTCTTTGGGGGAGAGCCATTGGTTTAAGCAAAAGATTAATGGCTTATGGAAT	900
QY	925	TGTGTTTTGTGCGCT 939	
Db	901	TGTGTTTTGTGCGCT 915	
<p>RESULT 13</p> <p>US-10-055-106C-1</p> <p>/ Sequence 1, Application US/10055106C</p> <p>/ Publication No. US20030017536A1</p> <p>/ GENERAL INFORMATION:</p> <p>/ APPLICANT: Pfizer Inc.</p> <p>/ APPLICANT: Harland, Lee</p> <p>/ TITLE OF INVENTION: Novel Polypeptide</p> <p>/ FILE REFERENCE: PCI0970AGLK</p> <p>/ CURRENT APPLICATION NUMBER: US/10/055,106C</p> <p>/ CURRENT FILING DATE: 2002-01-23</p> <p>/ PRIOR APPLICATION NUMBER: GB0101739.1</p> <p>/ PRIOR FILING DATE: 2001-01-23</p> <p>/ PRIOR APPLICATION NUMBER: US 60/267,341</p> <p>/ PRIOR FILING DATE: 2001-02-08</p> <p>/ NUMBER OF SEQ ID NOS: 3</p> <p>/ SOFTWARE: PatentIn version 3.1</p> <p>/ SEQ ID NO 1</p> <p>/ LENGTH: 918</p> <p>/ TYPE: DNA</p> <p>/ ORGANISM: Homo sapiens</p> <p>US-10-055-106C-1</p>			
<p>Query Match 97.3%; Score 913.4; DB 14; Length 918;</p> <p>Best Local Similarity 99.9%; Pred. No. 4.8e-263;</p> <p>Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>			
QY	25	ATGCGTCGACCAATATCCTCCAGGAATTCCTTTGCGATTCCTATATGTACACCCCACTTA	84
Db	1	ATGCGTCGACCAATATCCTCCAGGAATTCCTTTGCGATTCCTATATGTACACCCCACTTA	60
QY	85	ATGAGCCCTTACTCATATGTGCTTATTTGGCGGGCTGGTGGGTGTCAATTTCAATCTTTTC	144
Db	61	ATGAGCCCTTACTCATATGTGCTTATTTGGCGGGCTGGTGGGTGTCAATTTCAATCTTTTC	120



Db 841 CTCTCTTTGTCTTTGGGGAGACCATGTTGTTTAAGCAAAAGTAATTGGCTTAGGAAT 900  
QY 925 TGTGTTTGTGCCGT 939  
Db 901 TGTGTTTGTGCCGT 915

## RESULT 15

US-10-297-908A-2  
; Sequence 2, Application US/10297908A  
; Publication No. US20040029793A1  
; GENERAL INFORMATION:  
; APPLICANT: MORIYA, Takeo  
; APPLICANT: ITO, Takahashi  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: MIYAJIMA, No. US20040029793A1uyuki  
; TITLE OF INVENTION: No. US20040029793A1el G Protein-Coupled Receptor Protein and its  
; FILE REFERENCE: 2737 USOP  
; CURRENT APPLICATION NUMBER: US/10/297,908A  
; PRIOR FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/05061  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: JP 2000-184596  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: JP 2000-223887  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 2  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Human  
US-10-297-908A-2

Query Match 97.3%; Score 913.4; DB 17; Length 918;  
Best Local Similarity 99.9%; Pred. No. 4.8e-263;  
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATGCTGGGCCACATACCTCCAGGAATTCCTTTGCGATCTTAAGTGAACACCCCACTTA 84  
Db 1 ATGCTGGGCCACATACCTCCAGGAATTCCTTTGCGATCTTAAGTGAACACCCCACTTA 60  
QY 85 ATGAGCCTTACTTCAATAGTGTATTGAGCGGCGTGGTGGGTGCATTTTCATTTCTTTTC 144  
Db 61 ATGAGCCTTACTTCAATAGTGTATTGAGCGGCGTGGTGGGTGCATTTTCATTTCTTTTC 120  
QY 145 CTGCTGGTGAATGAACACCCGCTGAGTGAACCAACCATGGCGTCAATTAATCTGGTGTG 204  
Db 121 CTGCTGGTGAATGAACACCCGCTGAGTGAACCAACCATGGCGTCAATTAATCTGGTGTG 180  
QY 205 GTCACAGCGTTTTTCTGCTGACAGTGCATTTGCTTGAACCTACCTCATCAAGAAAGACT 264  
Db 181 GTCACAGCGTTTTTCTGCTGACAGTGCATTTGCTTGAACCTACCTCATCAAGAAAGACT 240  
QY 265 TGAATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGACATCAATGATAC 324  
Db 241 TGAATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGACATCAATGATAC 300  
QY 325 CTGACGTTCTATTCTAATGAGTGAATCCTGTGACCAAGATACCTCAATCTTCAAGTGC 384  
Db 301 CTGACGTTCTATTCTAATGAGTGAATCCTGTGACCAAGATACCTCAATCTTCAAGTGC 360  
QY 385 AAAGACAAAGTGAATCTACAGAAAATGCTGATGCTGTGCTGCCGGTATGGAATCCATGAGAA 504  
Db 361 AAAGACAAAGTGAATCTACAGAAAATGCTGATGCTGTGCTGCCGGTATGGAATCCATGAGAA 420  
QY 445 ACCGCTGATGATGTCATGTTGTGTAACCCGTGTTGTCTCCGGTATGGAATCCATGAGAA 504  
Db 421 ACCGCTGATGATGTCATGTTGTGTAACCCGTGTTGTCTCCGGTATGGAATCCATGAGAA 480  
QY 505 TACAATAGAGACATGTTTAAATTTCAAAAGAGCTTGTACATATATGGAATATC 564  
Db 481 TACAATAGAGACATGTTTAAATTTCAAAAGAGCTTGTACATATATGGAATATC 540

QY 565 ATCAACTATATGATAGTCATTTTGTGCATAGCCGTGCTGTGATTCGTGTGGCTTTCAG 624  
Db 541 ATCAACTATATGATAGTCATTTTGTGCATAGCCGTGCTGTGATTCGTGTGGCTTTCAG 600  
QY 625 GTCTTCATCATTAATGTTGATGTTGAGTGAAGTGAACGCACTCTTTACTATATCCACAGAG 684  
Db 601 GTCTTCATCATTAATGTTGATGTTGAGTGAAGTGAACGCACTCTTTACTATATCCACAGAG 660  
QY 685 TTCTGGGCTCAGCTGAAAACCTAATTTTATAGGGGTCATCCTGTTGTTCCCTCC 744  
Db 661 TTCTGGGCTCAGCTGAAAACCTAATTTTATAGGGGTCATCCTGTTGTTCCCTCC 720  
QY 745 TACAGTCTTTAGATCTATTACTTGAATGTTGAGCCGATTCATGCTGTGACAGC 804  
Db 721 TACAGTCTTTAGATCTATTACTTGAATGTTGAGCCGATTCATGCTGTGACAGC 780  
QY 805 AAGTTGCATTTTATACGAAAATCTTCTTGAAGTGAACGCAATTAAGCTGTATGATTTG 864  
Db 781 AAGTTGCATTTTATACGAAAATCTTCTTGAAGTGAACGCAATTAAGCTGTATGATTTG 840  
QY 865 CTTCCTTTGTCTTTGGGGGAGCCATGGTTTAAAGCAAAATATGGCTTAGGAAT 924  
Db 841 CTTCCTTTGTCTTTGGGGGAGCCATGGTTTAAAGCAAAATATGGCTTAGGAAT 900  
QY 925 TGTGTTTGTGCCGT 939  
Db 901 TGTGTTTGTGCCGT 915

Search completed: September 10, 2005, 03:39:15  
Job time : 679.311 secs